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SEQUENCE LISTING

<110> JAPAN SCIENCE AND TECHNOLOGY CORPORATION

<120> Screening of genes to give tolerance against
environmental stress and the applications

<130> 12-130

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<150> JP P1999-235910

<151> 1999-07-19

<150> JP P2000-85377

<151> 2000-03-24

<160> 66

<170> PatentIn Ver. 2.1

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<211> 1018

<212> DNA

<213> Bruguiera sexangula

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<221> CDS

<222> (42)..(464)

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Ser Ala Leu Arg Thr Val Ser Ser Ser Val Lys Val Val Gly Pro Ala

10

15

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Arg Ser Lys Ser Ala Thr Val Pro Thr Gln Thr Val Leu Pro Phe Lys

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30

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Phe Thr Asn Pro Ser Leu Leu Thr Arg Ser Leu Ser Phe Ser Ser Lys

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aga agc caa gcc act cca tct gal gal gcc tca aga ccc acc aaa gtt			296
Arg Ser Gln Ala Thr Pro Ser Asp Asp Ala Ser Arg Pro Thr Lys Val			
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caa gag ctg tgt gtg tat gag atg aac gag aga gal cgt gga agc cct			344
Gln Glu Leu Cys Val Tyr Glu Met Asn Glu Arg Asp Arg Gly Ser Pro			
90	95	100	
gct gtt ctg cgg ttg agc cag aaa cct gtt aat tct ctg ggc gal ctg			392
Ala Val Leu Arg Leu Ser Gln Lys Pro Val Asn Ser Leu Gly Asp Leu			
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Gly Val Thr Ala Glu Tyr Ala Ser			
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 <213> Bruguiera sexangula

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 Ser Phe Ser Ser Lys Gly Ser Ser Phe Asp Ser Phe Ser Val Pro Lys
 50 55 60
 Arg Ser Phe Ser Cys Arg Ser Gln Ala Thr Pro Ser Asp Asp Ala Ser
 65 70 75 80
 Arg Pro Thr Lys Val Gln Glu Leu Cys Val Tyr Glu Met Asn Glu Arg
 85 90 95
 Asp Arg Gly Ser Pro Ala Val Leu Arg Leu Ser Gln Lys Pro Val Asn
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Met Ala Ile Ala Ala Gln Thr Pro Asp Ile Leu	
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Gly Glu Arg Gln Ser Gly Gln Asp Val Arg Thr Gln Asn Val Val Ala	
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tgt caa gcg gtt gcc aat att gtc aaa tct tca ctt ggt cct gtc gga	209
Cys Gln Ala Val Ala Asn Ile Val Lys Ser Ser Leu Gly Pro Val Gly	
30 35 40	
ctc gac aag atg cta gtg gat gat att ggt gat gla aca att aca aat	257
Leu Asp Lys Met Leu Val Asp Asp Ile Gly Asp Val Thr Ile Thr Asn	
45 50 55	
gat ggt gct acg att ctt aag atg tta gaa gla gag cat cct gca gca	305
Asp Gly Ala Thr Ile Leu Lys Met Leu Glu Val Glu His Pro Ala Ala	
60 65 70 75	
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Lys Val Leu Val Glu Leu Ala Glu Leu Gln Asp Arg Glu Val Gly Asp	
80 85 90	
gga acc act tcc gtt gtc atc ata gca gct gag ttg ctc aag aga gca	401
Gly Thr Thr Ser Val Val Ile Ile Ala Ala Glu Leu Leu Lys Arg Ala	
95 100 105	
aat gat ctc gtg agg aat aag atc cac cca aca tca ata atc agt gga	449
Asn Asp Leu Val Arg Asn Lys Ile His Pro Thr Ser Ile Ile Ser Gly	
110 115 120	
tac agg ctt gct atg agg gaa gca tgc aag tat gtt gaa gag aaa ttg	497
Tyr Arg Leu Ala Met Arg Glu Ala Cys Lys Tyr Val Glu Glu Lys Leu	
125 130 135	
tca atg aag gtt gaa aag ctt gga aaa gat tct cta gla aac tgt gca	545
Ser Met Lys Val Glu Lys Leu Gly Lys Asp Ser Leu Val Asn Cys Ala	
140 145 150 155	
aag aca agc atg tcc tca aag ttg ata gct ggt gac agc gac ttc ttt	593
Lys Thr Ser Met Ser Ser Lys Leu Ile Ala Gly Asp Ser Asp Phe Phe	
160 165 170	
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Ala Asn Leu Val Val Asp Ala Val Gln Ala Val Lys Met Thr Asn Ala	

175	180	185	
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Arg Gly Glu Ile Lys Tyr Pro Ile Lys Ser Ile Asn Ile Leu Lys Ala			
190	195	200	
cat gga aaa agt gca aga gat agc tgc ctt ttg aat ggc tat gct ctc			737
His Gly Lys Ser Ala Arg Asp Ser Cys Leu Leu Asn Gly Tyr Ala Leu			
205	210	215	
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Asn Thr Gly Arg Ala Ala Gln Gly Met Pro Met Arg Val Ala Pro Ala			
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agg att gct tgt ctt gac ttt aat ctt cag aaa acg aag atg caa ttg			833
Arg Ile Ala Cys Leu Asp Phe Asn Leu Gln Lys Thr Lys Met Gln Leu			
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ggt gta caa gtc tta gtc acf gat ccc agg gag ctt gaa aga att cgt			881
Gly Val Gln Val Leu Val Thr Asp Pro Arg Glu Leu Glu Arg Ile Arg			
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caa aga gaa gct gat atg aca aag gaa cgg att gag aaa ctc ctg aaa			929
Gln Arg Glu Ala Asp Met Thr Lys Glu Arg Ile Glu Lys Leu Leu Lys			
270	275	280	
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Ala Gly Ala Asn Val Val Leu Thr Thr Lys Gly Ile Asp Asp Met Ala			
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aaa gag gat atg cgc cat gtt gcc aag gca acf ggt gca aca ctg gtt			1073
Lys Glu Asp Met Arg His Val Ala Lys Ala Thr Gly Ala Thr Leu Val			
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tca aca ttt gct gac atg gaa gga gag gaa aca ttt gat tca tca ctg			1121
Ser Thr Phe Ala Asp Met Glu Gly Glu Glu Thr Phe Asp Ser Ser Leu			
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glg att atg ala aaa ggg aca aag acf aca agf gcg gtt tcc ttg att	1217
Val Ile Met Ile Lys Gly Thr Lys Thr Thr Ser Ala Val Ser Leu Ile	
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380 385 390 395	
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His Asp Ala Leu Cys Ile Val Lys Arg Thr Leu Glu Ser Asn Thr Val	
400 405 410	
gtt gca ggt gga ggt gct gtt gag gct gcc ttg tct gtg cac ttg gag	1361
Val Ala Gly Gly Gly Ala Val Glu Ala Ala Leu Ser Val His Leu Glu	
415 420 425	
tac ctc gct aca acf ctt ggg tca cga gag cag tta gca ata gca gag	1409
Tyr Leu Ala Thr Thr Leu Gly Ser Arg Glu Gln Leu Ala Ile Ala Glu	
430 435 440	
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Phe Ala Glu Ser Leu Leu Ile Ile Pro Lys Val Leu Ala Val Asn Ala	
445 450 455	
gcc aaa gat gcc acf gaa tta gct gca aaa ctc cgg gct tac cac cat	1505
Ala Lys Asp Ala Thr Glu Leu Ala Ala Lys Leu Arg Ala Tyr His His	
460 465 470 475	
aca gca caa aca aag gct gat aag aaa cat tta tca agc atg gga cta	1553
Thr Ala Gln Thr Lys Ala Asp Lys Lys His Leu Ser Ser Met Gly Leu	
480 485 490	
gac ctt tca aag ggg acc atc cga aac aac tta gaa gct gga gtc att	1601
Asp Leu Ser Lys Gly Thr Ile Arg Asn Asn Leu Glu Ala Gly Val Ile	
495 500 505	
gaa cct gca atg agc aaa ata aag ata att cag ttt gct acf gaa gca	1649
Glu Pro Ala Met Ser Lys Ile Lys Ile Ile Gln Phe Ala Thr Glu Ala	
510 515 520	
gcc ala aca att ctt cga att gat gac atg atc aag ctt gtc aag gat	1697
Ala Ile Thr Ile Leu Arg Ile Asp Asp Met Ile Lys Leu Val Lys Asp	
525 530 535	
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Glu Thr Gln Asn Glu Glu Glu	

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545

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<212> PRT

<213> Bruguiera sexangula

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Asn	Ile	Val	Lys	Ser	Ser	Leu	Gly	Pro	Val	Gly	Leu	Asp	Lys	Met	Leu
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Val	Asp	Asp	Ile	Gly	Asp	Val	Thr	Ile	Thr	Asn	Asp	Gly	Ala	Thr	Ile
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Leu	Ala	Glu	Leu	Gln	Asp	Arg	Glu	Val	Gly	Asp	Gly	Thr	Thr	Ser	Val
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Asp Ala Val Gln Ala Val Lys Met Thr Asn Ala Arg Gly Glu Ile Lys		
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Tyr Pro Ile Lys Ser Ile Asn Ile Leu Lys Ala His Gly Lys Ser Ala		
195	200	205
Arg Asp Ser Cys Leu Leu Asn Gly Tyr Ala Leu Asn Thr Gly Arg Ala		
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Ala Gln Gly Met Pro Met Arg Val Ala Pro Ala Arg Ile Ala Cys Leu		
225	230	235 240
Asp Phe Asn Leu Gln Lys Thr Lys Met Gln Leu Gly Val Gln Val Leu		
245	250	255
Val Thr Asp Pro Arg Glu Leu Glu Arg Ile Arg Gln Arg Glu Ala Asp		
260	265	270
Met Thr Lys Glu Arg Ile Glu Lys Leu Leu Lys Ala Gly Ala Asn Val		
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Val Leu Thr Thr Lys Gly Ile Asp Asp Met Ala Leu Lys Tyr Phe Val		
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Glu Ala Gly Ala Ile Ala Val Arg Arg Val Arg Lys Glu Asp Met Arg		
305	310	315 320
His Val Ala Lys Ala Thr Gly Ala Thr Leu Val Ser Thr Phe Ala Asp		
325	330	335
Met Glu Gly Glu Glu Thr Phe Asp Ser Ser Leu Leu Gly Gln Ala Glu		
340	345	350
Glu Val Val Glu Glu Arg Ile Ala Asp Asp Asp Val Ile Met Ile Lys		
355	360	365
Gly Thr Lys Thr Thr Ser Ala Val Ser Leu Ile Leu Arg Gly Ala Asn		
370	375	380

Asp Tyr Met Leu Asp Glu Met Glu Arg Ala Leu His Asp Ala Leu Cys
 385 390 395 400
 Ile Val Lys Arg Thr Leu Glu Ser Asn Thr Val Val Ala Gly Gly Gly
 405 410 415
 Ala Val Glu Ala Ala Leu Ser Val His Leu Glu Tyr Leu Ala Thr Thr
 420 425 430
 Leu Gly Ser Arg Glu Gln Leu Ala Ile Ala Glu Phe Ala Glu Ser Leu
 435 440 445
 Leu Ile Ile Pro Lys Val Leu Ala Val Asn Ala Ala Lys Asp Ala Thr
 450 455 460
 Glu Leu Ala Ala Lys Leu Arg Ala Tyr His His Thr Ala Gln Thr Lys
 465 470 475 480
 Ala Asp Lys Lys His Leu Ser Ser Met Gly Leu Asp Leu Ser Lys Gly
 485 490 495
 Thr Ile Arg Asn Asn Leu Glu Ala Gly Val Ile Glu Pro Ala Met Ser
 500 505 510
 Lys Ile Lys Ile Ile Gln Phe Ala Thr Glu Ala Ala Ile Thr Ile Leu
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 Glu Glu
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 Gly Ala Ala Ser Lys Thr Gly Lys Leu Thr Leu Lys Thr Thr Glu Met
 20 25 30
 gag acg gtg tac gat ttg ggg gcg aaa atg ata gag gca ttg ggg aag 144
 Glu Thr Val Tyr Asp Leu Gly Ala Lys Met Ile Glu Ala Leu Gly Lys
 35 40 45
 gaa aag gtg cag agt ggg gat gtt att gca att gac aag gcg tcc ggc 192
 Glu Lys Val Gln Ser Gly Asp Val Ile Ala Ile Asp Lys Ala Ser Gly
 50 55 60
 aaa att aca aag cit ggg cgt tca ttt tct cgg tct agg gat tac gat 240
 Lys Ile Thr Lys Leu Gly Arg Ser Phe Ser Arg Ser Arg Asp Tyr Asp
 65 70 75 80
 gcc atg gga cca cag gtg aag ttt gtt cag tgc cct gat ggg gag ctg 288
 Ala Met Gly Pro Gln Val Lys Phe Val Gln Cys Pro Asp Gly Glu Leu
 85 90 95

cag aag agg aaa gag gtc glg cal lgl glc lca clg cac gag att gat	336
Gln Lys Arg Lys Glu Val Val His Cys Val Ser Leu His Glu Ile Asp	
100 105 110	
glt atc aat agc aga aca cag ggg ttt ctt gct ctt ttc acc ggg gat	384
Val Ile Asn Ser Arg Thr Gln Gly Phe Leu Ala Leu Phe Thr Gly Asp	
115 120 125	
act ggt gaa atc cgt gcg gag gtg agg gaa caa att gac aca aag gtg	432
Thr Gly Glu Ile Arg Ala Glu Val Arg Glu Gln Ile Asp Thr Lys Val	
130 135 140	
gct gaa tgg aga gag gaa ggg aaa gca gag att glg cca ggt glc ctc	480
Ala Glu Trp Arg Glu Glu Gly Lys Ala Glu Ile Val Pro Gly Val Leu	
145 150 155 160	
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Phe Ile Asp Glu Val His Met Leu Asp Ile Glu Cys Phe Ser Phe Leu	
165 170 175	
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180 185 190	
aac aga ggg atc acc aca atc aga ggc aca aat tac aaa tct cct cat	624
Asn Arg Gly Ile Thr Thr Ile Arg Gly Thr Asn Tyr Lys Ser Pro His	
195 200 205	
ggg att cca ata gat ctc ctt gat cga cta ctc att atc aca act caa	672
Gly Ile Pro Ile Asp Leu Leu Asp Arg Leu Leu Ile Ile Thr Thr Gln	
210 215 220	
cct tac aca aag gat gaa att cgt aag att ctg gat atc aga tgt cag	720
Pro Tyr Thr Lys Asp Glu Ile Arg Lys Ile Leu Asp Ile Arg Cys Gln	
225 230 235 240	
gaa gaa gat gtg gag atg gct gaa gag gca aag gct ttg tta aca cat	768
Glu Glu Asp Val Glu Met Ala Glu Glu Ala Lys Ala Leu Leu Thr His	
245 250 255	
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Ile Gly Ala Glu Thr Ser Leu Arg Tyr Ala Ile His Leu Ile Thr Ala	
260 265 270	
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Ala Ala Leu Ala Cys Gln Lys Arg Lys Gly Lys Leu Val Glu Thr Glu	

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Asp Ile Ser Arg Ala Tyr Asn Leu Phe Leu Asp Val Lys Arg Ser Thr			
290	295	300	
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Gln Tyr Leu Ile Glu Tyr Gln Asn Gln Tyr Met Phe Asn Glu Ala Pro			
305	310	315	320
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325	330		
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Glu Lys Val Gln Ser Gly Asp Val Ile Ala Ile Asp Lys Ala Ser Gly			
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Lys Ile Thr Lys Leu Gly Arg Ser Phe Ser Arg Ser Arg Asp Tyr Asp			
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Ala Met Gly Pro Gln Val Lys Phe Val Gln Cys Pro Asp Gly Glu Leu	85	90	95
Gln Lys Arg Lys Glu Val Val His Cys Val Ser Leu His Glu Ile Asp	100	105	110
Val Ile Asn Ser Arg Thr Gln Gly Phe Leu Ala Leu Phe Thr Gly Asp	115	120	125
Thr Gly Glu Ile Arg Ala Glu Val Arg Glu Gln Ile Asp Thr Lys Val	130	135	140
Ala Glu Trp Arg Glu Glu Gly Lys Ala Glu Ile Val Pro Gly Val Leu	145	150	155
Phe Ile Asp Glu Val His Met Leu Asp Ile Glu Cys Phe Ser Phe Leu	165	170	175
Asn Arg Ala Leu Glu Asn Glu Met Ala Pro Ile Leu Val Val Ala Thr	180	185	190
Asn Arg Gly Ile Thr Thr Ile Arg Gly Thr Asn Tyr Lys Ser Pro His	195	200	205
Gly Ile Pro Ile Asp Leu Leu Asp Arg Leu Leu Ile Ile Thr Thr Gln	210	215	220
Pro Tyr Thr Lys Asp Glu Ile Arg Lys Ile Leu Asp Ile Arg Cys Gln	225	230	235
Glu Glu Asp Val Glu Met Ala Glu Glu Ala Lys Ala Leu Leu Thr His	245	250	255
Ile Gly Ala Glu Thr Ser Leu Arg Tyr Ala Ile His Leu Ile Thr Ala	260	265	270
Ala Ala Leu Ala Cys Gln Lys Arg Lys Gly Lys Leu Val Glu Thr Glu	275	280	285
Asp Ile Ser Arg Ala Tyr Asn Leu Phe Leu Asp Val Lys Arg Ser Thr	290	295	300
Gln Tyr Leu Ile Glu Tyr Gln Asn Gln Tyr Met Phe Asn Glu Ala Pro	305	310	315
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 <213> *Bruguiera sexangula*

<220>
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 His Pro Lys Asn Tyr Gly Pro Gly Ser Arg Ala Cys Arg Val Cys Gly
 10 15 20 25

aat ccg cac ggg ttg atc agg aag tac gga ctc atg tgc tgc aga cag 149
 Asn Pro His Gly Leu Ile Arg Lys Tyr Gly Leu Met Cys Cys Arg Gln
 30 35 40

tgc ttc cgt agc aat gcc aag gaa att ggc ttc att aag tac cgc 194
 Cys Phe Arg Ser Asn Ala Lys Glu Ile Gly Phe Ile Lys Tyr Arg
 45 50 55

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ccccctcttc ggalgagcct taggacaaig ttcctcttag tttatgtatt gtigaacttg 314

gactgatgtt gaactaacga tatictgga tcalligata ttcgagagt ttattatttt 374

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 1 5
 att aac att gtg gtt att ggc cat gtc gac tcc gga aag tca acc aca 102
 Ile Asn Ile Val Val Ile Gly His Val Asp Ser Gly Lys Ser Thr Thr
 10 15 20
 act ggc cac ttg att tac aag ctt gga ggt atc gac aag cgt gtg att 150
 Thr Gly His Leu Ile Tyr Lys Leu Gly Gly Ile Asp Lys Arg Val Ile
 25 30 35
 gag agg ttt gag aag gaa gct gct gag atg aac aag agg tca ttc aag 198
 Glu Arg Phe Glu Lys Glu Ala Ala Glu Met Asn Lys Arg Ser Phe Lys
 40 45 50 55
 tat gcc tgg gtg ctt gac aag ctg aag gct gag cgt gag cgt ggt atc 246
 Tyr Ala Trp Val Leu Asp Lys Leu Lys Ala Glu Arg Glu Arg Gly Ile
 60 65 70
 acc att gat att gcc ttg tgg aag ttc gag aca acc aaa tat tac tgc 294
 Thr Ile Asp Ile Ala Leu Trp Lys Phe Glu Thr Thr Lys Tyr Tyr Cys
 75 80 85

acg gtc att gal gcl ccl gga cat cgl gac ttt att aag aat atg atc	342
Thr Val Ile Asp Ala Pro Gly His Arg Asp Phe Ile Lys Asn Met Ile	
90 95 100	
acc ggg act tcc caa gcl gac tgl gcl gtc ctc atc att gac tct acc	390
Thr Gly Thr Ser Gln Ala Asp Cys Ala Val Leu Ile Ile Asp Ser Thr	
105 110 115	
act ggt ggc ttt gag gcl ggt atc tct aaa gal ggt cag acc cgc gag	438
Thr Gly Gly Phe Glu Ala Gly Ile Ser Lys Asp Gly Gln Thr Arg Glu	
120 125 130 135	
cat gcc ctg ctt gcc ttc acc ctt ggt gtt aag caa atg att tgc tgc	486
His Ala Leu Leu Ala Phe Thr Leu Gly Val Lys Gln Met Ile Cys Cys	
140 145 150	
tgc aac aag atg gal gcl acc act tcc aag tat tct aag gca aga tat	534
Cys Asn Lys Met Asp Ala Thr Thr Ser Lys Tyr Ser Lys Ala Arg Tyr	
155 160 165	
gal gaa att gtt aag gaa gtg tca tcc tac ttg aag aag gtt ggt tac	582
Asp Glu Ile Val Lys Glu Val Ser Ser Tyr Leu Lys Lys Val Gly Tyr	
170 175 180	
aac cca gag aag att cct ttt gtc ccc ata tct gga ttt gag ggt gac	630
Asn Pro Glu Lys Ile Pro Phe Val Pro Ile Ser Gly Phe Glu Gly Asp	
185 190 195	
aac atg att gag aga tcc acc aac ctt gac tgg tac aag ggc cca act	678
Asn Met Ile Glu Arg Ser Thr Asn Leu Asp Trp Tyr Lys Gly Pro Thr	
200 205 210 215	
ctt ctt gag gcc ctg gac atg atc cag gag cca aag agg cca tca gat	726
Leu Leu Glu Ala Leu Asp Met Ile Gln Glu Pro Lys Arg Pro Ser Asp	
220 225 230	
aag ccc ctc cgt ctc cca ctt cag gal glg tac aag att ggt ggt att	774
Lys Pro Leu Arg Leu Pro Leu Gln Asp Val Tyr Lys Ile Gly Gly Ile	
235 240 245	
ggg aca gtc cca glg ggt cgt gtt gaa act ggt gtc ctg aag cct gga	822
Gly Thr Val Pro Val Gly Arg Val Glu Thr Gly Val Leu Lys Pro Gly	
250 255 260	
atg gtt gtt act ttt ggt ccc tca gga ctg acc act gaa gtt aag tct	870

Met	Val	Val	Thr	Phe	Gly	Pro	Ser	Gly	Leu	Thr	Thr	Glu	Val	Lys	Ser		
265						270					275						
gtg	gag	atg	cac	cat	gaa	gct	ctc	caa	gag	gct	ctt	ccc	gga	gac	aac	918	
Val	Glu	Met	His	His	Glu	Ala	Leu	Gln	Glu	Ala	Leu	Pro	Gly	Asp	Asn		
280					285				290						295		
glt	ggc	ttc	aat	glt	aag	aat	glt	tcc	glg	aag	gat	ctt	aag	cgg	ggt	966	
Val	Gly	Phe	Asn	Val	Lys	Asn	Val	Ser	Val	Lys	Asp	Leu	Lys	Arg	Gly		
			300					305					310				
tat	glt	gcc	tca	aac	tcc	aag	gat	gat	ccf	gcc	aag	gag	gca	tcf	agc	1014	
Tyr	Val	Ala	Ser	Asn	Ser	Lys	Asp	Asp	Pro	Ala	Lys	Glu	Ala	Ser	Ser		
			315					320					325				
ttc	acc	tcc	caa	glt	atc	atc	atg	aac	cac	ccf	ggt	cag	att	gga	aaf	1062	
Phe	Thr	Ser	Gln	Val	Ile	Ile	Met	Asn	His	Pro	Gly	Gln	Ile	Gly	Asn		
			330				335					340					
ggt	tat	gcc	ccf	glt	ctg	gat	tgc	cac	acc	tcf	cac	att	gct	gtc	aag	1110	
Gly	Tyr	Ala	Pro	Val	Leu	Asp	Cys	His	Thr	Ser	His	Ile	Ala	Val	Lys		
	345					350					355						
ttt	tcf	gag	atc	ctc	aca	aag	att	gat	agg	cga	tcf	ggc	aag	gag	ctt	1158	
Phe	Ser	Glu	Ile	Leu	Thr	Lys	Ile	Asp	Arg	Arg	Ser	Gly	Lys	Glu	Leu		
360					365				370					375			
gaa	aag	gag	ccc	aag	ttc	ttg	aag	aat	ggt	gat	gct	ggg	ttc	gtg	aag	1206	
Glu	Lys	Glu	Pro	Lys	Phe	Leu	Lys	Asn	Gly	Asp	Ala	Gly	Phe	Val	Lys		
			380						385				390				
atg	att	ccg	acc	aag	ccf	atg	gtg	gtg	gaa	act	ttc	tcc	gag	tat	ccf	1254	
Met	Ile	Pro	Thr	Lys	Pro	Met	Val	Val	Glu	Thr	Phe	Ser	Glu	Tyr	Pro		
			395					400					405				
ccg	ctt	ggt	aga	ttt	gcc	gtc	agg	gac	atg	cgc	cag	act	glt	gca	gtg	1302	
Pro	Leu	Gly	Arg	Phe	Ala	Val	Arg	Asp	Met	Arg	Gln	Thr	Val	Ala	Val		
			410				415					420					
gga	gtc	atc	aag	agt	gtc	gag	aaa	aag	gaa	ccf	tcf	gga	gct	aag	gtg	1350	
Gly	Val	Ile	Lys	Ser	Val	Glu	Lys	Lys	Glu	Pro	Ser	Gly	Ala	Lys	Val		
	425					430					435						
act	aaa	tcf	gct	gcc	aag	aag	ggt	ggc	aaa	lgaaccgtgc	aaglcagagt					1400	
Thr	Lys	Ser	Ala	Ala	Lys	Lys	Gly	Gly	Lys								
440						445											

tgaatgagat gaaggctatt ggaagaataa agacggggcc ctggtagcg gcttaattat 1460
 tggatgttca gcagttgggt tggagaacta cagtttcaat tcagcgccat calcacggag 1520
 ctgtgttcc cagaattggg ttcttgaccg tgggtggcat tggctgttgg tttagatgac 1580
 ttctttgtgt catgtttaga cttaacgga ttgctattt calaaagcgg ctggggaatt 1640
 ttaaaaaaaaa aaaaaaaaaa aaaa 1664

<210> 12
 <211> 449
 <212> PRT
 <213> Bruguiera sexangula

<400> 12
 Met Gly Lys Glu Lys Ile His Ile Asn Ile Val Val Ile Gly His Val
 1 5 10 15
 Asp Ser Gly Lys Ser Thr Thr Thr Gly His Leu Ile Tyr Lys Leu Gly
 20 25 30
 Gly Ile Asp Lys Arg Val Ile Glu Arg Phe Glu Lys Glu Ala Ala Glu
 35 40 45
 Met Asn Lys Arg Ser Phe Lys Tyr Ala Trp Val Leu Asp Lys Leu Lys
 50 55 60
 Ala Glu Arg Glu Arg Gly Ile Thr Ile Asp Ile Ala Leu Trp Lys Phe
 65 70 75 80
 Glu Thr Thr Lys Tyr Tyr Cys Thr Val Ile Asp Ala Pro Gly His Arg
 85 90 95
 Asp Phe Ile Lys Asn Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala
 100 105 110
 Val Leu Ile Ile Asp Ser Thr Thr Gly Gly Phe Glu Ala Gly Ile Ser
 115 120 125
 Lys Asp Gly Gln Thr Arg Glu His Ala Leu Leu Ala Phe Thr Leu Gly
 130 135 140
 Val Lys Gln Met Ile Cys Cys Cys Asn Lys Met Asp Ala Thr Thr Ser

145		150		155		160
Lys Tyr Ser Lys Ala Arg Tyr Asp Glu Ile Val Lys Glu Val Ser Ser						
	165		170		175	
Tyr Leu Lys Lys Val Gly Tyr Asn Pro Glu Lys Ile Pro Phe Val Pro						
	180		185		190	
Ile Ser Gly Phe Glu Gly Asp Asn Met Ile Glu Arg Ser Thr Asn Leu						
	195		200		205	
Asp Trp Tyr Lys Gly Pro Thr Leu Leu Glu Ala Leu Asp Met Ile Gln						
	210		215		220	
Glu Pro Lys Arg Pro Ser Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp						
	225		230		235	240
Val Tyr Lys Ile Gly Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu						
	245		250		255	
Thr Gly Val Leu Lys Pro Gly Met Val Val Thr Phe Gly Pro Ser Gly						
	260		265		270	
Leu Thr Thr Glu Val Lys Ser Val Glu Met His His Glu Ala Leu Gln						
	275		280		285	
Glu Ala Leu Pro Gly Asp Asn Val Gly Phe Asn Val Lys Asn Val Ser						
	290		295		300	
Val Lys Asp Leu Lys Arg Gly Tyr Val Ala Ser Asn Ser Lys Asp Asp						
	305		310		315	320
Pro Ala Lys Glu Ala Ser Ser Phe Thr Ser Gln Val Ile Ile Met Asn						
	325		330		335	
His Pro Gly Gln Ile Gly Asn Gly Tyr Ala Pro Val Leu Asp Cys His						
	340		345		350	
Thr Ser His Ile Ala Val Lys Phe Ser Glu Ile Leu Thr Lys Ile Asp						
	355		360		365	
Arg Arg Ser Gly Lys Glu Leu Glu Lys Glu Pro Lys Phe Leu Lys Asn						
	370		375		380	
Gly Asp Ala Gly Phe Val Lys Met Ile Pro Thr Lys Pro Met Val Val						
	385		390		395	400

Glu Thr Phe Ser Glu Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp
 405 410 415

Met Arg Gln Thr Val Ala Val Gly Val Ile Lys Ser Val Glu Lys Lys
 420 425 430

Glu Pro Ser Gly Ala Lys Val Thr Lys Ser Ala Ala Lys Lys Gly Gly
 435 440 445

Lys

<210> 13

<211> 770

<212> DNA

<213> *Bruguiera sexangula*

<220>

<221> CDS

<222> (2).. (769)

<400> 13

c gat gat atg gac gag gcc aca ccc acc ttt gtt tgg ggc acc aat atc 49
 Asp Asp Met Asp Glu Ala Thr Pro Thr Phe Val Trp Gly Thr Asn Ile
 1 5 10 15

agc gtc cag gat gtc aag gcc gct att cag atg ttt ttg aag cac ttc 97
 Ser Val Gln Asp Val Lys Ala Ala Ile Gln Met Phe Leu Lys His Phe
 20 25 30

agg gat agt aat cag agt caa agg aac gag att ttt gaa gaa ggg aag 145
 Arg Asp Ser Asn Gln Ser Gln Arg Asn Glu Ile Phe Glu Glu Gly Lys
 35 40 45

tac gtc aaa gcg ata cat aag gtt ctt gaa gtt gaa gga gag tcg ctt 193
 Tyr Val Lys Ala Ile His Lys Val Leu Glu Val Glu Gly Glu Ser Leu
 50 55 60

gat gtt gat gct cgt gat gtc ttt gat tat gat tct gat ttg tat gcc 241
 Asp Val Asp Ala Arg Asp Val Phe Asp Tyr Asp Ser Asp Leu Tyr Ala
 65 70 75 80

aag atg att cgg tac cca ctt gag gtt ttg gcc att ttc gac att gtt 289

Lys Met Ile Arg Tyr Pro Leu Glu Val Leu Ala Ile Phe Asp Ile Val	
85 90 95	
ttg atg gat att glg agt ttg atc aac cct ttg ttt gag aaa cat gta	337
Leu Met Asp Ile Val Ser Leu Ile Asn Pro Leu Phe Glu Lys His Val	
100 105 110	
caa gtc agg att ttc aat ctt aag acc tgc att aca atg aga aat ctc	385
Gln Val Arg Ile Phe Asn Leu Lys Thr Ser Ile Thr Met Arg Asn Leu	
115 120 125	
aac cct tct gat atc gaa aag atg gtc tca ttg aag gga atg ala att	433
Asn Pro Ser Asp Ile Glu Lys Met Val Ser Leu Lys Gly Met Ile Ile	
130 135 140	
cgg tgt agt tcc ala ala ccg gag atc agg gaa gca gta ttt aga tgc	481
Arg Cys Ser Ser Ile Ile Pro Glu Ile Arg Glu Ala Val Phe Arg Cys	
145 150 155 160	
ctt gtt tgt ggc tac ttc tct gat ccc atc gtt gtg gat aga gga cgg	529
Leu Val Cys Gly Tyr Phe Ser Asp Pro Ile Val Val Asp Arg Gly Arg	
165 170 175	
ata agt gaa cct aaa gca tgc ttg aaa gag gaa tgt ctt act aag aac	577
Ile Ser Glu Pro Lys Ala Cys Leu Lys Glu Glu Cys Leu Thr Lys Asn	
180 185 190	
tcc atg aca cta gtt cac aat cgt tgc agg ttt gct gat aag cag att	625
Ser Met Thr Leu Val His Asn Arg Cys Arg Phe Ala Asp Lys Gln Ile	
195 200 205	
gtg agg ctc cag gag aca cct gac gag atc cct gaa gga gga aca cca	673
Val Arg Leu Gln Glu Thr Pro Asp Glu Ile Pro Glu Gly Gly Thr Pro	
210 215 220	
cac acg gtg agc tta ttg atg cat gac aag ctg gta gat gct gga aag	721
His Thr Val Ser Leu Leu Met His Asp Lys Leu Val Asp Ala Gly Lys	
225 230 235 240	
cca ggt gac agg gtt gag gtc act gga att tat agg gct atg agt gtt a	770
Pro Gly Asp Arg Val Glu Val Thr Gly Ile Tyr Arg Ala Met Ser Val	
245 250 255	

<210> 14
<211> 256

<212> PRT

<213> *Bruguiera sexangula*

<400> 14

Asp Asp Met Asp Glu Ala Thr Pro Thr Phe Val Trp Gly Thr Asn Ile
1 5 10 15

Ser Val Gln Asp Val Lys Ala Ala Ile Gln Met Phe Leu Lys His Phe
20 25 30

Arg Asp Ser Asn Gln Ser Gln Arg Asn Glu Ile Phe Glu Glu Gly Lys
35 40 45

Tyr Val Lys Ala Ile His Lys Val Leu Glu Val Glu Gly Glu Ser Leu
50 55 60

Asp Val Asp Ala Arg Asp Val Phe Asp Tyr Asp Ser Asp Leu Tyr Ala
65 70 75 80

Lys Met Ile Arg Tyr Pro Leu Glu Val Leu Ala Ile Phe Asp Ile Val
85 90 95

Leu Met Asp Ile Val Ser Leu Ile Asn Pro Leu Phe Glu Lys His Val
100 105 110

Gln Val Arg Ile Phe Asn Leu Lys Thr Ser Ile Thr Met Arg Asn Leu
115 120 125

Asn Pro Ser Asp Ile Glu Lys Met Val Ser Leu Lys Gly Met Ile Ile
130 135 140

Arg Cys Ser Ser Ile Ile Pro Glu Ile Arg Glu Ala Val Phe Arg Cys
145 150 155 160

Leu Val Cys Gly Tyr Phe Ser Asp Pro Ile Val Val Asp Arg Gly Arg
165 170 175

Ile Ser Glu Pro Lys Ala Cys Leu Lys Glu Glu Cys Leu Thr Lys Asn
180 185 190

Ser Met Thr Leu Val His Asn Arg Cys Arg Phe Ala Asp Lys Gln Ile
195 200 205

Val Arg Leu Gln Glu Thr Pro Asp Glu Ile Pro Glu Gly Gly Thr Pro
210 215 220

His Thr Val Ser Leu Leu Met His Asp Lys Leu Val Asp Ala Gly Lys
 225 230 235 240

Pro Gly Asp Arg Val Glu Val Thr Gly Ile Tyr Arg Ala Met Ser Val
 245 250 255

<210> 15

<211> 846

<212> DNA

<213> Mesembryanthemum crystallinum

<220>

<221> CDS

<222> (39).. (530)

<400> 15

caaatlilct ttgcigaalc gaatctacaa. aataccig atg ggt cag gtt ctt gac 56
 Met Gly Gln Val Leu Asp
 1 5

aaa ttt caa cgt aag caa tgg aga caa aag caa atc cag aag ata aca 104
 Lys Phe Gln Arg Lys Gln Trp Arg Gln Lys Gln Ile Gln Lys Ile Thr
 10 15 20

gat aag gla ttt gat cgt gtc aaa agt ccg acc gga aat ggc act ctt 152
 Asp Lys Val Phe Asp Arg Val Lys Ser Pro Thr Gly Asn Gly Thr Leu
 25 30 35

aca ttt gaa gag ctg tat ata gct acc ctg att gtc tac aat gat ata 200
 Thr Phe Glu Glu Leu Tyr Ile Ala Thr Leu Ile Val Tyr Asn Asp Ile
 40 45 50

aac aag tat ttg ccg ggg ccg cac ttt gat cct cca tcg aaa gac aaa 248
 Asn Lys Tyr Leu Pro Gly Pro His Phe Asp Pro Pro Ser Lys Asp Lys
 55 60 65 70

atc aga gcc ttg atg cag gaa tgc gat atg gat gtc gat gga gaa ctt 296
 Ile Arg Ala Leu Met Gln Glu Cys Asp Met Asp Val Asp Gly Glu Leu
 75 80 85

aac cgt gag gaa ttt glg aag ttc atg cag aag glg aca gcc gat aca 344
 Asn Arg Glu Glu Phe Val Lys Phe Met Gln Lys Val Thr Ala Asp Thr
 90 95 100

ttc tct acg gtc agc cag gga ctg att atc tct ctg att ctg gcg cca 392
 Phe Ser Thr Val Ser Gln Gly Leu Ile Ile Ser Leu Ile Leu Ala Pro
 105 110 115

aca gtt gca ttg gcg acg aag agg gca aca gaa ggt gtt cca ggt gtg 440
 Thr Val Ala Leu Ala Thr Lys Arg Ala Thr Glu Gly Val Pro Gly Val
 120 125 130

ggg aaa gtg gtg caa aag gtg cct act tca att tat gca tcc ctg gtg 488
 Gly Lys Val Val Gln Lys Val Pro Thr Ser Ile Tyr Ala Ser Leu Val
 135 140 145 150

acc ctt gtt gtc gtt gca atc caa act gct agc gag gga tgc 530
 Thr Leu Val Val Val Ala Ile Gln Thr Ala Ser Glu Gly Cys
 155 160

tgattagagg ctttagttac ttgttcatga tacagaagga acagtttgg tcaattttatt 590

tcitttttttaa taggacataa ggaagttgta tatctttctt ctctcttcta ccaggttttg 650

ggggaagttg gaaagaacat acaaatgatt tcaactgcgt atggcctgat cctccatttt 710

attaaaactt gtcgtgtcta gcatgagcga ttcaataattt gcaataatgca atatttgtaa 770

tgaatgtctac attcagtgat tagtgigatt gtgcagtttg ttgggaaaaa aaaaaaaaaa 830

aaaaaaaaa aaaaaa 846

<210> 16

<211> 164

<212> PRT

<213> Mesembryanthemum crystallinum

<400> 16

Met Gly Gln Val Leu Asp Lys Phe Gln Arg Lys Gln Trp Arg Gln Lys

1

5

10

15

Gln Ile Gln Lys Ile Thr Asp Lys Val Phe Asp Arg Val Lys Ser Pro

20

25

30

Thr Gly Asn Gly Thr Leu Thr Phe Glu Glu Leu Tyr Ile Ala Thr Leu

35

40

45

Ile Val Tyr Asn Asp Ile Asn Lys Tyr Leu Pro Gly Pro His Phe Asp

50

55

60

Pro Pro Ser Lys Asp Lys Ile Arg Ala Leu Met Gln Glu Cys Asp Met
 65 70 75 80
 Asp Val Asp Gly Glu Leu Asn Arg Glu Glu Phe Val Lys Phe Met Gln
 85 90 95
 Lys Val Thr Ala Asp Thr Phe Ser Thr Val Ser Gln Gly Leu Ile Ile
 100 105 110
 Ser Leu Ile Leu Ala Pro Thr Val Ala Leu Ala Thr Lys Arg Ala Thr
 115 120 125
 Glu Gly Val Pro Gly Val Gly Lys Val Val Gln Lys Val Pro Thr Ser
 130 135 140
 Ile Tyr Ala Ser Leu Val Thr Leu Val Val Val Ala Ile Gln Thr Ala
 145 150 155 160
 Ser Glu Gly Cys

<210> 17
 <211> 872
 <212> DNA
 <213> Mesembryanthemum crystallinum

<220>
 <221> CDS
 <222> (183).. (569)

<400> 17
 aacaaaatgt ctcctctctt ctcctctctt ttcctctctt ctcctctctt gggcttgattg 60
 agtaagctct gtcctcttgc tctctgttga atgtactatc tctctgtgaac caaaggccaa 120
 agattaacia ttggagattt ctcctactcga aatttctttt taggtgttga cctctgttgag 180
 ct atg gcg aac aag ccc caa att cca acg aag aat tct gcc ctc att 227
 Met Ala Asn Lys Pro Gln Ile Pro Thr Lys Asn Ser Ala Leu Ile
 1 5 10 15
 gct att atc gcg gat gag gat act gla act gga ttt ttg ctg gct gga 275
 Ala Ile Ile Ala Asp Glu Asp Thr Val Thr Gly Phe Leu Leu Ala Gly

	20	25	30	
glt ggt aat gtt gat cta cga aga cag aca aat tac att att glg gac				323
Val Gly Asn Val Asp Leu Arg Arg Gln Thr Asn Tyr Ile Ile Val Asp				
	35	40	45	
aat aaa aca acg atg aag caa atc gaa gat gca ttc aag gag ttc aca				371
Asn Lys Thr Thr Met Lys Gln Ile Glu Asp Ala Phe Lys Glu Phe Thr				
	50	55	60	
gca aga gag gac att gcg gtt gla cta atc agc caa tat gtt-gca aat				419
Ala Arg Glu Asp Ile Ala Val Val Leu Ile Ser Gln Tyr Val Ala Asn				
	65	70	75	
atg ata aga gta ttg gtt gat agc tac aac aaa cca atc ccg gca att				467
Met Ile Arg Val Leu Val Asp Ser Tyr Asn Lys Pro Ile Pro Ala Ile				
	80	85	90	95
ttg gag att cct tca aag gac cat cct tat gat cct aac cat gat tca				515
Leu Glu Ile Pro Ser Lys Asp His Pro Tyr Asp Pro Asn His Asp Ser				
	100	105	110	
gtc ctt tca agg gtt aaa tac ctg ttc tct tct gaa tcg gca tca agc				563
Val Leu Ser Arg Val Lys Tyr Leu Phe Ser Ser Glu Ser Ala Ser Ser				
	115	120	125	
aga ttt tagccataag ctttgtaaag ttccctgcct ctgaatgttt ggtagattaag				619
Arg Phe				
agtttaaaact agaaccagtc acattctgac ttggatattt gaggcactgt ttgttttaag				679
ttcttaaaat aaggagtgta attacgacac calgaatcgg gatatgacac calgaatcgc				739
atgtatttct ttccatctca ttgaaagag tggagcagcc atatcatlta gtltcttcc				799
cttgcgaatg agcttgggaag aaatgttttg gctataaaag atttcaactc ttggtacaaa				859
aaaaaaaaa aaa				872

<210> 18

<211> 129

<212> PRT

<213> Mesembryanthemum crystallinum

<400> 18

Met Ala Asn Lys Pro Gln Ile Pro Thr Lys Asn Ser Ala Leu Ile Ala
 1 5 10 15
 Ile Ile Ala Asp Glu Asp Thr Val Thr Gly Phe Leu Leu Ala Gly Val
 20 25 30
 Gly Asn Val Asp Leu Arg Arg Gln Thr Asn Tyr Ile Ile Val Asp Asn
 35 40 45
 Lys Thr Thr Met Lys Gln Ile Glu Asp Ala Phe Lys Glu Phe Thr Ala
 50 55 60
 Arg Glu Asp Ile Ala Val Val Leu Ile Ser Gln Tyr Val Ala Asn Met
 65 70 75 80
 Ile Arg Val Leu Val Asp Ser Tyr Asn Lys Pro Ile Pro Ala Ile Leu
 85 90 95
 Glu Ile Pro Ser Lys Asp His Pro Tyr Asp Pro Asn His Asp Ser Val
 100 105 110
 Leu Ser Arg Val Lys Tyr Leu Phe Ser Ser Glu Ser Ala Ser Ser Arg
 115 120 125
 Phe

<210> 19
 <211> 647
 <212> DNA
 <213> Mesembryanthemum crystallinum

<220>
 <221> CDS
 <222> (64)..(426)

<400> 19
 cllgltttc tctctccctc tctctctctc tctccgcacc ctcaggcagt gaaggtagca 60

aca atg gcg tac gcg atg aag cca acg aag ccc ggg atg gag gaa tcc 108
 Met Ala Tyr Ala Met Lys Pro Thr Lys Pro Gly Met Glu Glu Ser
 1 5 10 15

cag gag cag att cac aag atc agg atc act ctt tct tct aag aac gtc 156

	20		25		30										
Asn	Leu	Glu	Lys	Val	Cys	Ala	Asp	Leu	Val	Arg	Gly	Ala	Lys	Asp	Lys
	35						40					45			
Arg	Leu	Arg	Val	Lys	Gly	Pro	Val	Arg	Met	Pro	Thr	Lys	Val	Leu	Lys
	50					55					60				
Ile	Thr	Thr	Arg	Lys	Ser	Pro	Cys	Gly	Glu	Gly	Thr	Asn	Thr	Phe	Asp
	65				70				75					80	
Arg	Phe	Glu	Leu	Arg	Val	His	Lys	Arg	Val	Ile	Asp	Leu	Phe	Ser	Ser
				85					90					95	
Pro	Asp	Val	Val	Lys	Gln	Ile	Thr	Ser	Ile	Thr	Ile	Glu	Pro	Gly	Val
		100						105					110		
Glu	Val	Glu	Val	Thr	Ile	Ala	Asp	Ser							
		115					120								

<210> 21
 <211> 686
 <212> DNA
 <213> Sueada japonica

<220>
 <221> CDS
 <222> (62)..(493)

<400> 21
 acaccattca caaaacacat taataaaaaa cactacttct ttctttctta gccacttgaa 60
 a aig gcc tac tca aag gct gta ctc ctt gcc ctt atc ttt gct gtg act 109
 Met Ala Tyr Ser Lys Ala Val Leu Leu Ala Leu Ile Phe Ala Val Thr
 1 5 10 15
 ctt gtc att gcc tct cag gtc tca gct cgt gaa ctt gct gag gag aca 157
 Leu Val Ile Ala Ser Gln Val Ser Ala Arg Glu Leu Ala Glu Glu Thr
 20 25 30
 caa tct gtg gag gag tct aag gga tac ggt ggt ggg cac gga ggt cac 205
 Gln Ser Val Glu Glu Ser Lys Gly Tyr Gly Gly Gly His Gly Gly His
 35 40 45

tat ggt ggt ggt cac tat ggt ggt gga cac aga cac ggt ggc cat gga 253
 Tyr Gly Gly Gly His Tyr Gly Gly Gly His Arg His Gly Gly His Gly
 50 55 60

cac tac gca act gag gaa gca gag aac aag aat gaa gcc gla gaa cct 301
 His Tyr Ala Thr Glu Glu Ala Glu Asn Lys Asn Glu Ala Val Glu Pro
 65 70 75 80

caa ggc ggc tat ggt cac gga cac gga gga ggc tac gga cac ggt ggt 349
 Gln Gly Gly Tyr Gly His Gly His Gly Gly Tyr Gly His Gly Gly
 85 90 95

ggc tac gga cac ggt gga ggc tac gga cac gga ggt ggc tac ggg cac 397
 Gly Tyr Gly His Gly Gly Gly Tyr Gly His Gly Gly Gly Tyr Gly His
 100 105 110

ggt ggt ggc tac gga cat gga ggt ggt tat gga cac ggt gga cac ggt 445
 Gly Gly Gly Tyr Gly His Gly Gly Gly Tyr Gly His Gly Gly His Gly
 115 120 125

gga cat ggt ggt cat ggt cac tac gcc aag act acc gag gaa caa aat 493
 Gly His Gly Gly His Gly His Tyr Ala Lys Thr Thr Glu Glu Gln Asn
 130 135 140

taagtatatggtttactaaaa cttaaattgt acgttgtcaa ataaaaatgta ctttatgatt 553

ttacatgagt atgcatgtaa ttacatcaaa gcttcaagga ctatcttgta ctttatgta 613

tatacciaata tgaatggaa gcgtgacttt tattactgta aaaaaaaaaa aaaaaaaaaa 673

aaaaaaaaaa aaa 686

<210> 22

<211> 144

<212> PRT

<213> Sueada japonica

<400> 22

Met Ala Tyr Ser Lys Ala Val Leu Leu Ala Leu Ile Phe Ala Val Thr
 1 5 10 15

Leu Val Ile Ala Ser Gln Val Ser Ala Arg Glu Leu Ala Glu Glu Thr
 20 25 30

Gln Ser Val Glu Glu Ser Lys Gly Tyr Gly Gly Gly His Gly Gly His

	40	45	50	
acg gtg agg tgc agc gcc tgc aag agg cca aac cta tgc aac agg tca				248
Thr Val Arg Cys Ser Ala Ser Lys Arg Pro Asn Leu Cys Asn Arg Ser				
	55	60	65	
lgt ggc agt lgt tgc aag acg tgc aac tgc glg cca cca ggc act tcc				296
Cys Gly Ser Cys Cys Lys Thr Cys Asn Cys Val Pro Pro Gly Thr Ser				
	70	75	80	
ggc aac tac gaa gcc tgc cct lgt tac gcc aac ttg acc acc cac ggc				344
Gly Asn Tyr Glu Ala Cys Pro Cys Tyr Ala Asn Leu Thr Thr His Gly				
	85	90	95	
aat cga cac aag tgc cct taattaaaca gaattgttta gtgttttatt				392
Asn Arg His Lys Cys Pro				
100	105			
acaaccgtac caatgaacgt acicclattt acactactag agtactagta ataaacattt				452
ttaggcacgg tccagltgtt caatgagcta gtggatattt gagtcaaaa tgagtattg				512
aaaatgagat atgataaaaag tglattatct acattgtagt actgttttgt atcatagtgt				572
agtatgttt attttctgta ccttaattt gtlactttgt attccctttc attctatcta				632
tttacaatcc ttttgaagt ttatgtgaaa aaaaaaaaaa aaaaaaaaaa a				683

<210> 24
 <211> 105
 <212> PRT
 <213> Salsola komarovii

<400> 24
 Met Ala Phe Ser Lys Pro Leu Ile Ala Ser Leu Leu Leu Ser Leu Phe
 1 5 10 15
 Val Leu Gln Phe Val His Ala Val Glu Pro Ile Ser Ser Ser Asn Gln
 20 25 30
 Val Gly Ser Asn Thr Gly Gly Thr Ser Glu Ser Lys Val Asp Cys Gly
 35 40 45
 Ala Ala Cys Thr Val Arg Cys Ser Ala Ser Lys Arg Pro Asn Leu Cys
 50 55 60

Asn Arg Ser Cys Gly Ser Cys Cys Lys Thr Cys Asn Cys Val Pro Pro
 65 70 75 80
 Gly Thr Ser Gly Asn Tyr Glu Ala Cys Pro Cys Tyr Ala Asn Leu Thr
 85 90 95
 Thr His Gly Asn Arg His Lys Cys Pro
 100 105

<210> 25
 <211> 803
 <212> DNA
 <213> Salsola komarovii

<220>
 <221> CDS
 <222> (51).. (593)

<400> 25
 cgcagacgcl tcagtccltt ctcctccttt ctcctcctc accgigaaag atg ggg 56
 Met Gly
 1
 ttg tca ttt acc aaa ttg ttt agc cgg ttg ttc gct aag aag gaa atg 104
 Leu Ser Phe Thr Lys Leu Phe Ser Arg Leu Phe Ala Lys Lys Glu Met
 5 10 15
 cgt atc ctt atg gtc ggt ctc gat gcc gct ggt aaa acc acc att ctc 152
 Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr Ile Leu
 20 25 30
 tat aaa ctc aag ctg gga gag att gtc acc acc att cct acc att gga 200
 Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr Ile Gly
 35 40 45 50
 ttt aat gtg gag act gla gaa tac aag aac atc agc ttc act gtg tgg 248
 Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr Val Trp
 55 60 65
 gat gtc ggg ggt caa gac aag att cgt cca ttg tgg aga cal tac ttc 296
 Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His Tyr Phe
 70 75 80

caa aac acc caa ggi ctc atc ttt gtg gtt gac agt aat gal cgt gac 344
Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp Arg Asp
85 90 95

cgt gtc gtt gag gca aga gal gaa ctg cal agg atg tta aat gag gal 392
Arg Val Val Glu Ala Arg Asp Glu Leu His Arg Met Leu Asn Glu Asp
100 105 110

gaa tta cga gat gca gig ttg ttg gtg ttt gca aac aag caa gat ctt 440
Glu Leu Arg Asp Ala Val Leu Leu Val Phe Ala Asn Lys Gln Asp Leu
115 120 125 130

ccc aat gca atg aat gct gct gag atc act gal aag ctt ggt ctc cal 488
Pro Asn Ala Met Asn Ala Ala Glu Ile Thr Asp Lys Leu Gly Leu His
135 140 145

tct cta cgt caa cgc cal tgg tac ata caa agc aca tgt gcc acc tct 536
Ser Leu Arg Gln Arg His Trp Tyr Ile Gln Ser Thr Cys Ala Thr Ser
150 155 160

gga gaa ggg ctt tac gag ggt ctg gac tgg ctc tca aac aat atc gct 584
Gly Glu Gly Leu Tyr Glu Gly Leu Asp Trp Leu Ser Asn Asn Ile Ala
165 170 175

agc aag gct taaaagtaac agaacgagta aggttagctt tcicagagaa 633
Ser Lys Ala
180

gaagctggag tataggciga ggactatcgt tactgctagt gtlacccttt ttatttttgc 693

catllatalg ttacatttt tggttcctat cggacaagaa ttattttctg cgtttatgtt 753

gacttgttat aataccatcac tttttagttg aaaaaaaaaa aaaaaaaaaa 803

<210> 26

<211> 181

<212> PRT

<213> Salsola komarovii

<400> 26

Met Gly Leu Ser Phe Thr Lys Leu Phe Ser Arg Leu Phe Ala Lys Lys
1 5 10 15

Glu Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr
20 25 30

Ile Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr
 35 40 45
 Ile Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr
 50 55 60
 Val Trp Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His
 65 70 75 80
 Tyr Phe Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp
 85 90 95
 Arg Asp Arg Val Val Glu Ala Arg Asp Glu Leu His Arg Met Leu Asn
 100 105 110
 Glu Asp Glu Leu Arg Asp Ala Val Leu Leu Val Phe Ala Asn Lys Gln
 115 120 125
 Asp Leu Pro Asn Ala Met Asn Ala Ala Glu Ile Thr Asp Lys Leu Gly
 130 135 140
 Leu His Ser Leu Arg Gln Arg His Trp Tyr Ile Gln Ser Thr Cys Ala
 145 150 155 160
 Thr Ser Gly Glu Gly Leu Tyr Glu Gly Leu Asp Trp Leu Ser Asn Asn
 165 170 175
 Ile Ala Ser Lys Ala
 180

<210> 27

<211> 680

<212> DNA

<213> Avicennia marina

<220>

<221> CDS

<222> (161).. (454)

<400> 27

ctaaaagcca aaggcaagat aagaacagg ttcccttagc tatcttctc gtcctgcctc 60

tgcaaaaggt ccatccccag aagatcagga aaacctctct gcagcagcac tctaataatc 120

Asn Glu Ile Ser Ala Leu Val Thr Arg Arg Gly Tyr Ala Ala Leu Ala
 20 25 30
 Gln Gly Val Val Ser Ser Ser Ala Arg Ser Gly Gly Ala Pro Asn Val
 35 40 45
 Met Leu Lys Lys Gly Ser Glu Glu Ser Gly Lys Thr Ala Trp Val Pro
 50 55 60
 Asp Pro Asp Thr Gly Tyr Tyr Arg Pro Gly Asn Glu Asp Lys Ala Ala
 65 70 75 80
 Leu Asp Pro Val Glu Leu Arg Glu Met Leu Ile Lys Asn Lys Pro Ser
 85 90 95
 Arg Gln

<210> 29
 <211> 490
 <212> DNA
 <213> *Avicennia marina*

<220>
 <221> CDS
 <222> (20).. (349)

<400> 29
 tcggctgggc aaagaaggg atg gcg att cca tcg gaa att cgg gac ttt att 52
 Met Ala Ile Pro Ser Glu Ile Arg Asp Phe Ile
 1 5 10

 gct agc cgc aac aga tct ttg gtg atc gca tct cca aag gaa gat gag 100
 Ala Ser Arg Asn Arg Ser Leu Val Ile Ala Ser Pro Lys Glu Asp Glu
 15 20 25

 aaa att ctc cgc tca agg cag tgc acc gaa gaa ggg gcg cgt gca gga 148
 Lys Ile Leu Arg Ser Arg Gln Cys Thr Glu Glu Gly Ala Arg Ala Gly
 30 35 40

 gcc aaa gct gct gca gtt gct tgc gtt gcc agc gcc att ccc act cgt 196
 Ala Lys Ala Ala Ala Val Ala Cys Val Ala Ser Ala Ile Pro Thr Leu
 45 50 55

gta gct gtt cga acg att ccg tgg gca aag gca aac ctc aac tat aca 244
Val Ala Val Arg Thr Ile Pro Trp Ala Lys Ala Asn Leu Asn Tyr Thr
60 65 70 75

gcc cag gca ctc att ata tct tct gca tcc ata gcg gca tac ttt atc 292
Ala Gln Ala Leu Ile Ile Ser Ser Ala Ser Ile Ala Ala Tyr Phe Ile
80 85 90

gct gct gac aaa acc atc tta gag tgc gca cgg aaa aat gca gag tac 340
Ala Ala Asp Lys Thr Ile Leu Glu Cys Ala Arg Lys Asn Ala Glu Tyr
95 100 105

aaa tct gct taagatgatg tgaagacaa tgtgtcagc ttgcaatgct 389
Lys Ser Ala
110

tgcctatgact tgtgtttatg tgtatttcaa gtttctgaaa ctgcatttt gattttgtgt 449

tcctaatgcaa tgagcattat ggaaaaaaaa aaaaaaaaaa a 490

<210> 30

<211> 110

<212> PRT

<213> Avicennia marina

<400> 30

Met Ala Ile Pro Ser Glu Ile Arg Asp Phe Ile Ala Ser Arg Asn Arg
1 5 10 15

Ser Leu Val Ile Ala Ser Pro Lys Glu Asp Glu Lys Ile Leu Arg Ser
20 25 30

Arg Gln Cys Thr Glu Glu Gly Ala Arg Ala Gly Ala Lys Ala Ala Ala
35 40 45

Val Ala Cys Val Ala Ser Ala Ile Pro Thr Leu Val Ala Val Arg Thr
50 55 60

Ile Pro Trp Ala Lys Ala Asn Leu Asn Tyr Thr Ala Gln Ala Leu Ile
65 70 75 80

Ile Ser Ser Ala Ser Ile Ala Ala Tyr Phe Ile Ala Ala Asp Lys Thr
85 90 95

Ile Leu Glu Cys Ala Arg Lys Asn Ala Glu Tyr Lys Ser Ala
100 105 110

<210> 31
<211> 592
<212> DNA
<213> Avicennia marina

<220>
<221> CDS
<222> (75)..(320)

<400> 31
gcagtcacag cctccctgct cccclggcgc ctccaaatll glgaalllcl cgagtgctaa 60
aagattcagc caag atg cag aac gaa gag ggg caa aac atg gal ctc tac 110
Met Gln Asn Glu Glu Gly Gln Asn Met Asp Leu Tyr
1 5 10
atc ccc agg aaa tgc tct gcc acg aac agg ctg atc acc tcc aag gat 158
Ile Pro Arg Lys Cys Ser Ala Thr Asn Arg Leu Ile Thr Ser Lys Asp
15 20 25
cat gct tct gtc cag atc aat gtt ggg cac ttg gat gag aat ggc cga 206
His Ala Ser Val Gln Ile Asn Val Gly His Leu Asp Glu Asn Gly Arg
30 35 40
tac act ggc caa tac tct acc ttt gct ctt tgt gga ttc atc cgt gct 254
Tyr Thr Gly Gln Tyr Ser Thr Phe Ala Leu Cys Gly Phe Ile Arg Ala
45 50 55 60
cag ggt gal gct gac agt gct ctt gal agg ctc tgg cag aaa aag aaa 302
Gln Gly Asp Ala Asp Ser Ala Leu Asp Arg Leu Trp Gln Lys Lys Lys
65 70 75
glc gaa acc agg cag cag tgalccctgct caattcagca gtgaaagitt 350
Val Glu Thr Arg Gln Gln
80
tttgggtttt gtctctgtgt gtgttatllt tgcctttcca gaatcaattt ctgtactgga 410
ttgagttatla aaaatgigga gclaaagggt gggagacctg atgcccittgt tactcgagla 470
atcacaagta galactgggc ttglaaatagc glgataatlg tgccttgcctc ttgcccatal 530

gactacgaat cagllaatgag allagacaat gllaatclcc aaaaaaaaaa aaaaaaaaaa 590

aa 592

<210> 32

<211> 82

<212> PRT

<213> Avicennia marina

<400> 32

Met Gln Asn Glu Glu Gly Gln Asn Met Asp Leu Tyr Ile Pro Arg Lys
1 5 10 15

Cys Ser Ala Thr Asn Arg Leu Ile Thr Ser Lys Asp His Ala Ser Val
20 25 30

Gln Ile Asn Val Gly His Leu Asp Glu Asn Gly Arg Tyr Thr Gly Gln
35 40 45

Tyr Ser Thr Phe Ala Leu Cys Gly Phe Ile Arg Ala Gln Gly Asp Ala
50 55 60

Asp Ser Ala Leu Asp Arg Leu Trp Gln Lys Lys Lys Val Glu Thr Arg
65 70 75 80

Gln Gln

<210> 33

<211> 1806

<212> DNA

<213> Avicennia marina

<220>

<221> CDS

<222> (362)..(1552)

<400> 33

tgtagaggta aagctacag catattcgc gccgcicgtt tgattacgtg ttgcctttat 60

ttgggaattt gatagcgcig agtagccgat gccgcicggag ggtaattgtt attttaggaa 120

tacgggtttg ttgattcgc agttttacig tctctagggt tgggccctga ggcttctggg 180
 atttgggatt taatcgciga tcaacagtt tcttgagaa aatattctta gtgcgcaat 240
 atctgatttg ctgacgagaa attgalacac ggttatgcga ttgagttttg ttgctgcaa 300
 agatattcgg agtgcctgct agatgtggat aatccggagg gctgtttcga tgagatgagg 360
 g atg tta tca ggg tta atg aac ttc ctg tgg gcc tgt ttt cgg cca agg 409
 Met Leu Ser Gly Leu Met Asn Phe Leu Trp Ala Cys Phe Arg Pro Arg
 1 5 10 15
 gcg gat cga agt gtt cac acg ggt tca gat gca ggc ggt cgt cag gat 457
 Ala Asp Arg Ser Val His Thr Gly Ser Asp Ala Gly Gly Arg Gln Asp
 20 25 30
 ggg ctt tta tgg tat aag gac ttg ggg caa cat atc aat gga gag ttt 505
 Gly Leu Leu Trp Tyr Lys Asp Leu Gly Gln His Ile Asn Gly Glu Phe
 35 40 45
 tca atg gct gia gtt caa gca aat aac tta cta gag gat cag agt caa 553
 Ser Met Ala Val Val Gln Ala Asn Asn Leu Leu Glu Asp Gln Ser Gln
 50 55 60
 ctt gaa tct ggt tgc ctg agc ttg agt gat tca gga caa tat ggc act 601
 Leu Glu Ser Gly Cys Leu Ser Leu Ser Asp Ser Gly Gln Tyr Gly Thr
 65 70 75 80
 ttt gtg ggg att tat gat gga cat gga ggt cct gag acc tct cgg ttt 649
 Phe Val Gly Ile Tyr Asp Gly His Gly Gly Pro Glu Thr Ser Arg Phe
 85 90 95
 atc aat gac cat ctc ttc caa cat ata aag aga ttc aca gct gag cat 697
 Ile Asn Asp His Leu Phe Gln His Ile Lys Arg Phe Thr Ala Glu His
 100 105 110
 caa tca atg tca gct gag gtc att cac aag gcc att caa gcg act gaa 745
 Gln Ser Met Ser Ala Glu Val Ile His Lys Ala Ile Gln Ala Thr Glu
 115 120 125
 gaa ggt ttt ttc tgc gtt gtt agc aga caa tgg tcc atg caa cca cag 793
 Glu Gly Phe Phe Ser Val Val Ser Arg Gln Trp Ser Met Gln Pro Gln
 130 135 140
 att gca gca gtt ggc tct tgc tgc ctt gtt ggt gtc atc tgt agt ggc 841
 Ile Ala Ala Val Gly Ser Cys Cys Leu Val Gly Val Ile Cys Ser Gly

145	150	155	160	
act ctt tat gtt tcc aac ctt ggt gat tcc cgt gct gtt ctt ggg acg				889
Thr Leu Tyr Val Ser Asn Leu Gly Asp Ser Arg Ala Val Leu Gly Thr				
	165	170	175	
ctt tcc aag gct aca ggg gaa gla cag gct act caa ctc tca aca gag				937
Leu Ser Lys Ala Thr Gly Glu Val Gln Ala Thr Gln Leu Ser Thr Glu				
	180	185	190	
cat aat gca agt ttt gag tct gtg aga cgg gaa ctg cag tct ctg cac				985
His Asn Ala Ser Phe Glu Ser Val Arg Arg Glu Leu Gln Ser Leu His				
	195	200	205	
cca gat gac tca cag att gtg gtt cta aag cat aat gta tgg cga gtg				1033
Pro Asp Asp Ser Gln Ile Val Val Leu Lys His Asn Val Trp Arg Val				
	210	215	220	
aag ggt ctt ata cag atc tca aga tca att gga gat gtg tat ttg aaa				1081
Lys Gly Leu Ile Gln Ile Ser Arg Ser Ile Gly Asp Val Tyr Leu Lys				
	225	230	235	240
aag gct gaa ttc aac agg gag cct cta tat cag aaa ttt cga ctt cgt				1129
Lys Ala Glu Phe Asn Arg Glu Pro Leu Tyr Gln Lys Phe Arg Leu Arg				
	245	250	255	
gaa gct ttc aaa aga cca att ttg agc tca gaa cca gaa act act gtg				1177
Glu Ala Phe Lys Arg Pro Ile Leu Ser Ser Glu Pro Glu Thr Thr Val				
	260	265	270	
cac cag ctg ctg cct cat gat caa ttc att atc ttc gca tca gat ggc				1225
His Gln Leu Leu Pro His Asp Gln Phe Ile Ile Phe Ala Ser Asp Gly				
	275	280	285	
ctt tgg gag cac ctt tcc aac caa gaa gca gtt gat ctt gtt cag aaa				1273
Leu Trp Glu His Leu Ser Asn Gln Glu Ala Val Asp Leu Val Gln Lys				
	290	295	300	
cat cca cac aat ggg att gct aga aga tta gla aaa gca gct ttg caa				1321
His Pro His Asn Gly Ile Ala Arg Arg Leu Val Lys Ala Ala Leu Gln				
	305	310	315	320
gag gca gca aag aaa agg gaa atg agg tac tcg gat ttg aag aaa att				1369
Glu Ala Ala Lys Lys Arg Glu Met Arg Tyr Ser Asp Leu Lys Lys Ile				
	325	330	335	

gac cgl ggg gll cgc cgl cal ltc cal gal gac atc acf gtl glg glg 1417
 Asp Arg Gly Val Arg Arg His Phe His Asp Asp Ile Thr Val Val Val
 340 345 350
 glg lll cll gac tca cac cll glg agc cgg gcl agc tca glc cgg ggc 1465
 Val Phe Leu Asp Ser His Leu Val Ser Arg Ala Ser Ser Val Arg Gly
 355 360 365
 cca aac atc tcc glg aaa ggl ggc ggc atc agt clg ccl ccc aat gcl 1513
 Pro Asn Ile Ser Val Lys Gly Gly Gly Ile Ser Leu Pro Pro Asn Ala
 370 375 380
 cll gca ccl tgl gcc aca cca acg gag cca glc cca aat lgatclgcl 1562
 Leu Ala Pro Cys Ala Thr Pro Thr Glu Pro Val Pro Asn
 385 390 395
 glclcllclla algtlaltlc ccgllagtlc lgtlglacfa lltllaalglg aatacaggta 1622
 gcllcllaac ggataacagc ggcccltgaa lcllllaalc calacigtaa cllllaaccg 1682
 gagaclallla cltggcalag llccaatgcc caaggatcac alagaciggg acaagccalc 1742
 tlggcggllga caatcalcal agllaaglll lclgggcata lclllcaaaa aaaaaaaaaa 1802
 aaaa 1806

<210> 34
 <211> 397
 <212> PRT
 <213> Avicennia marina

<400> 34
 Met Leu Ser Gly Leu Met Asn Phe Leu Trp Ala Cys Phe Arg Pro Arg
 1 5 10 15
 Ala Asp Arg Ser Val His Thr Gly Ser Asp Ala Gly Gly Arg Gln Asp
 20 25 30
 Gly Leu Leu Trp Tyr Lys Asp Leu Gly Gln His Ile Asn Gly Glu Phe
 35 40 45
 Ser Met Ala Val Val Gln Ala Asn Asn Leu Leu Glu Asp Gln Ser Gln
 50 55 60
 Leu Glu Ser Gly Cys Leu Ser Leu Ser Asp Ser Gly Gln Tyr Gly Thr

65		70		75		80									
Phe	Val	Gly	Ile	Tyr	Asp	Gly	His	Gly	Gly	Pro	Glu	Thr	Ser	Arg	Phe
			85					90						95	
Ile	Asn	Asp	His	Leu	Phe	Gln	His	Ile	Lys	Arg	Phe	Thr	Ala	Glu	His
			100					105					110		
Gln	Ser	Met	Ser	Ala	Glu	Val	Ile	His	Lys	Ala	Ile	Gln	Ala	Thr	Glu
		115					120					125			
Glu	Gly	Phe	Phe	Ser	Val	Val	Ser	Arg	Gln	Trp	Ser	Met	Gln	Pro	Gln
	130					135					140				
Ile	Ala	Ala	Val	Gly	Ser	Cys	Cys	Leu	Val	Gly	Val	Ile	Cys	Ser	Gly
145				150					155						160
Thr	Leu	Tyr	Val	Ser	Asn	Leu	Gly	Asp	Ser	Arg	Ala	Val	Leu	Gly	Thr
			165					170						175	
Leu	Ser	Lys	Ala	Thr	Gly	Glu	Val	Gln	Ala	Thr	Gln	Leu	Ser	Thr	Glu
		180						185					190		
His	Asn	Ala	Ser	Phe	Glu	Ser	Val	Arg	Arg	Glu	Leu	Gln	Ser	Leu	His
		195					200					205			
Pro	Asp	Asp	Ser	Gln	Ile	Val	Val	Leu	Lys	His	Asn	Val	Trp	Arg	Val
	210					215					220				
Lys	Gly	Leu	Ile	Gln	Ile	Ser	Arg	Ser	Ile	Gly	Asp	Val	Tyr	Leu	Lys
225				230					235						240
Lys	Ala	Glu	Phe	Asn	Arg	Glu	Pro	Leu	Tyr	Gln	Lys	Phe	Arg	Leu	Arg
				245					250					255	
Glu	Ala	Phe	Lys	Arg	Pro	Ile	Leu	Ser	Ser	Glu	Pro	Glu	Thr	Thr	Val
			260					265					270		
His	Gln	Leu	Leu	Pro	His	Asp	Gln	Phe	Ile	Ile	Phe	Ala	Ser	Asp	Gly
		275					280					285			
Leu	Trp	Glu	His	Leu	Ser	Asn	Gln	Glu	Ala	Val	Asp	Leu	Val	Gln	Lys
	290					295					300				
His	Pro	His	Asn	Gly	Ile	Ala	Arg	Arg	Leu	Val	Lys	Ala	Ala	Leu	Gln
305				310						315					320

65	70	75	80	
gca acg ttt ttg aaa ggc gct gtt gtt tat gaa gla aag tat tgt gct				288
Ala Thr Phe Leu Lys Gly Ala Val Val Tyr Glu Val Lys Tyr Cys Ala				
	85	90	95	
tat tca caa gca aca aga cgc atc agc tat gga gaa ggc gag tca ttt				336
Tyr Ser Gln Ala Thr Arg Arg Ile Ser Tyr Gly Glu Gly Glu Ser Phe				
	100	105	110	
act gct ggt acc ttt cag ttg gtc act gcc tca gac caa acc ggt att				384
Thr Ala Gly Thr Phe Gln Leu Val Thr Ala Ser Asp Gln Thr Gly Ile				
	115	120	125	
ggt tac tac aca tct agc agc ttg tct gat ggt gla tgacttatcg				430
Gly Tyr Tyr Thr Ser Ser Ser Leu Ser Asp Gly Val				
	130	135	140	
gaactcccca gtttctgcat tctgaaaggt gctttttgat ttccgaataa ttcttcaaat				490
ccacatgta gaagatccat tctttaggtc agatgtctat ctactgcctc cagccttag				550
ctgcctatgg gtattgggtc ccttctatit ttaggtagag tctttgagta agccttgcca				610
calcaaggcc tcagattatt gaatglacaa cagaataggt tglagcttca ttggctagta				670
cagtgacctc ttctatgggt ctgaaacatc aatataaagg ttgaaatggc aaaaaaaaaa				730
aaaaaaaaa aaa				743

<210> 36

<211> 140

<212> PRT

<213> Mesembryanthemum crystallinum

<400> 36

Pro	Glu	Leu	Ala	Pro	Lys	Asp	Gly	Asp	Phe	Arg	Phe	Asn	Ile	Ser	Glu
1				5				10					15		

Leu	Glu	Ala	Met	Leu	Pro	Ala	Gly	Thr	Val	Asp	His	Ala	Val	Glu	Arg
			20				25						30		

Ile	Tyr	Gln	Glu	Met	Pro	Arg	Trp	Glu	Glu	Thr	Val	Leu	Gly	Ser	Arg
			35				40					45			

Ser Arg Tyr Glu His Val Ile Gln Ala Leu Ala Asp Lys Tyr Pro Ser
 50 55 60
 Glu Asn Leu Leu Leu Val Thr His Gly Glu Gly Val Gly Thr Ser Val
 65 70 75 80
 Ala Thr Phe Leu Lys Gly Ala Val Val Tyr Glu Val Lys Tyr Cys Ala
 85 90 95
 Tyr Ser Gln Ala Thr Arg Arg Ile Ser Tyr Gly Glu Gly Glu Ser Phe
 100 105 110
 Thr Ala Gly Thr Phe Gln Leu Val Thr Ala Ser Asp Gln Thr Gly Ile
 115 120 125
 Gly Tyr Tyr Thr Ser Ser Ser Leu Ser Asp Gly Val
 130 135 140

<210> 37
 <211> 348
 <212> DNA
 <213> Sueada japonica

<220>
 <221> CDS
 <222> (1).. (246)

<400> 37
 atc att gct ccc cta gct att ggt ttg atc gtt ggt gcc aac atc tta 48
 Ile Ile Ala Pro Leu Ala Ile Gly Leu Ile Val Gly Ala Asn Ile Leu
 1 5 10 15
 gcc gga ggt gca ttt gat ggt gcc tca atg aac cct gcc gtc tct ttt 96
 Ala Gly Gly Ala Phe Asp Gly Ala Ser Met Asn Pro Ala Val Ser Phe
 20 25 30
 ggc ccc gcc gtg gtt agc tgg agc tgg gcc aac cac tgg gtc tac tgg 144
 Gly Pro Ala Val Val Ser Trp Ser Trp Ala Asn His Trp Val Tyr Trp
 35 40 45
 gca ggc cca ctc att ggt ggt gga ctt gct ggt ctc gtt tat gag ttt 192
 Ala Gly Pro Leu Ile Gly Gly Gly Leu Ala Gly Leu Val Tyr Glu Phe
 50 55 60

alc lll att ggt cac caa gag cca gcl lcc gcl gac iac cag aga ctc 240
 lle phe lle gly his gln glu pro ala ser ala asp tyr gln arg leu
 65 70 75 80

lcl gcl laagaallll aatlclllgc cclagggaaa aatglilcal gcalgtalll 296
 Ser Ala

lgtlatlllg lgggtlclaa aatlllatga agggaaaaaa aaaaaaaaaa aa 348

<210> 38

<211> 82

<212> PRT

<213> Sueada japonica

<400> 38

lle lle ala pro leu ala lle gly leu lle val gly ala asn lle leu
 1 5 10 15

ala gly gly ala phe asp gly ala ser met asn pro ala val ser phe
 20 25 30

gly pro ala val val ser trp ser trp ala asn his trp val tyr trp
 35 40 45

ala gly pro leu lle gly gly gly leu ala gly leu val tyr glu phe
 50 55 60

lle phe lle gly his gln glu pro ala ser ala asp tyr gln arg leu
 65 70 75 80

Ser Ala

<210> 39

<211> 1602

<212> DNA

<213> Sueada japonica

<220>

<221> CDS

<222> (1).. (1419)

<400> 39

cac acc gtt gal tta acc att gaa gct atg atg ctc gat tct caa gct	48
His Thr Val Asp Leu Thr Ile Glu Ala Met Met Leu Asp Ser Gln Ala	
1 5 10 15	
tct gat ctt gac aaa gaa gaa cgt cct gag att ctt tca atg ctt ccg	96
Ser Asp Leu Asp Lys Glu Glu Arg Pro Glu Ile Leu Ser Met Leu Pro	
20 25 30	
cct ctt gaa gga aaa tgc ctc ttg gaa ctt ggg gct ggt att ggt cgt	144
Pro Leu Glu Gly Lys Cys Leu Leu Glu Leu Gly Ala Gly Ile Gly Arg	
35 40 45	
ttt act ggt gaa ttg gct gag aaa gct ggc cag gtt att gct ctg gat	192
Phe Thr Gly Glu Leu Ala Glu Lys Ala Gly Gln Val Ile Ala Leu Asp	
50 55 60	
ttc att gag agt gct atc aag aag aat gaa gla atc aat ggg cac tac	240
Phe Ile Glu Ser Ala Ile Lys Lys Asn Glu Val Ile Asn Gly His Tyr	
65 70 75 80	
aaa aat gtc aag ttt atg tgt gct gat gtg act tct ccc act ctc agt	288
Lys Asn Val Lys Phe Met Cys Ala Asp Val Thr Ser Pro Thr Leu Ser	
85 90 95	
ttc cca cca cat tca ttg gat gtg ala ttc tcc aat tgg tta ctc atg	336
Phe Pro Pro His Ser Leu Asp Val Ile Phe Ser Asn Trp Leu Leu Met	
100 105 110	
tat ctt tct gat gaa gag gtg gaa aat ttg gtt gaa aga atg ttg aaa	384
Tyr Leu Ser Asp Glu Glu Val Glu Asn Leu Val Glu Arg Met Leu Lys	
115 120 125	
tgg ttg aag cca ggg ggt tac att ttc ttc aga gaa tct tgt ttc cat	432
Trp Leu Lys Pro Gly Gly Tyr Ile Phe Phe Arg Glu Ser Cys Phe His	
130 135 140	
caa tct ggg gat cac aaa cgc aaa agc aat ccc acc cac tac cgt gaa	480
Gln Ser Gly Asp His Lys Arg Lys Ser Asn Pro Thr His Tyr Arg Glu	
145 150 155 160	
cct agg ttc tac act aag gcc ttc aaa gag tgt cat ttg caa gat gga	528
Pro Arg Phe Tyr Thr Lys Ala Phe Lys Glu Cys His Leu Gln Asp Gly	
165 170 175	
tct gga aac tct tat gag ctc tcc cta ctt agc tgc aaa tgt att gga	576
Ser Gly Asn Ser Tyr Glu Leu Ser Leu Leu Ser Cys Lys Cys Ile Gly	

180	185	190	
gct tat gtc aga aac aag aaa aac cag aac cag att agt tgg ttg tgg			624
Ala Tyr Val Arg Asn Lys Lys Asn Gln Asn Gln Ile Ser Trp Leu Trp			
195	200	205	
caa aaa gtt gat tct aag gat gat aag ggg ttc cag cga ttt ctg gat			672
Gln Lys Val Asp Ser Lys Asp Asp Lys Gly Phe Gln Arg Phe Leu Asp			
210	215	220	
act agc cag tac aag tgt aat agc att ctg cga tat gag cgt gta ttt			720
Thr Ser Gln Tyr Lys Cys Asn Ser Ile Leu Arg Tyr Glu Arg Val Phe			
225	230	235	240
ggc cct ggt tat gtt agc act gga gga tat gaa acc acc aaa gag ttt			768
Gly Pro Gly Tyr Val Ser Thr Gly Gly Tyr Glu Thr Thr Lys Glu Phe			
245	250	255	
gtg tca atg ctg gac ttg aag cct ggc cag aag gtc ctg gat gtt ggt			816
Val Ser Met Leu Asp Leu Lys Pro Gly Gln Lys Val Leu Asp Val Gly			
260	265	270	
tgt gga att ggt gga ggt gac ttt tac atg gcg gag acc ttt gat gtt			864
Cys Gly Ile Gly Gly Gly Asp Phe Tyr Met Ala Glu Thr Phe Asp Val			
275	280	285	
gag gtt gtt gga ttt gat ctg tcc gtt aat atg att tcc ttt gcc ctt			912
Glu Val Val Gly Phe Asp Leu Ser Val Asn Met Ile Ser Phe Ala Leu			
290	295	300	
gag cgt tct att ggg ctt aaa tgt gct gtt gag ttt gag gla gca gat			960
Glu Arg Ser Ile Gly Leu Lys Cys Ala Val Glu Phe Glu Val Ala Asp			
305	310	315	320
tgc acc aag ata aac tac cct gat aac tct ttt gat gtc atc tat agc			1008
Cys Thr Lys Ile Asn Tyr Pro Asp Asn Ser Phe Asp Val Ile Tyr Ser			
325	330	335	
cgt gac acc att ctg cat att cag gac aag cct gcg ttg ttt aga tcc			1056
Arg Asp Thr Ile Leu His Ile Gln Asp Lys Pro Ala Leu Phe Arg Ser			
340	345	350	
ttc tac aaa tgg ttg aag cca gga ggt aaa gtt cta atc agt gat tac			1104
Phe Tyr Lys Trp Leu Lys Pro Gly Gly Lys Val Leu Ile Ser Asp Tyr			
355	360	365	

tgc aag aaa gct ggt cca ccc tca cct gaa ttc gcc gct tac att aag 1152
 Cys Lys Lys Ala Gly Pro Pro Ser Pro Glu Phe Ala Ala Tyr Ile Lys
 370 375 380

cag agg gga tat gat ctc cat gat gla aag gaa tat ggg cag atg ctt 1200
 Gln Arg Gly Tyr Asp Leu His Asp Val Lys Glu Tyr Gly Gln Met Leu
 385 390 395 400

aaa gat gct gga ttt gtt gat gtt ctt gcc gag gat aga act gag cag 1248
 Lys Asp Ala Gly Phe Val Asp Val Leu Ala Glu Asp Arg Thr Glu Gln
 405 410 415

ttc att cga gtt cta cgg aag gaa cta gag act gtt gag aag gaa aag 1296
 Phe Ile Arg Val Leu Arg Lys Glu Leu Glu Thr Val Glu Lys Glu Lys
 420 425 430

gat gtg ttc att agt gat ttc tct gag gag gat tac aat gac att gtt 1344
 Asp Val Phe Ile Ser Asp Phe Ser Glu Glu Asp Tyr Asn Asp Ile Val
 435 440 445

gga ggt igg aat gat aag ttg cgg agg act gcc aag ggt gag caa cga 1392
 Gly Gly Trp Asn Asp Lys Leu Arg Arg Thr Ala Lys Gly Glu Gln Arg
 450 455 460

tgg ggt ctg ttc gtt gcc aag aag aag tgaagaatca gttagccgcac 1439
 Trp Gly Leu Phe Val Ala Lys Lys Lys
 465 470

tggcactgtc gatctcctag tattaatctt caatgttttc aigtatgta ctctacatg 1499

taaaatlgcc aataagttgc atttcgcaga ctgtaagaig attaatcata ttttatcttt 1559

taattaatca tggatttatg caaaaaaaaaa aaaaaaaaaa aaa 1602

<210> 40
 <211> 473
 <212> PRT
 <213> Suecda japonica

<400> 40
 His Thr Val Asp Leu Thr Ile Glu Ala Met Met Leu Asp Ser Gln Ala
 1 5 10 15
 Ser Asp Leu Asp Lys Glu Glu Arg Pro Glu Ile Leu Ser Met Leu Pro
 20 25 30

Pro	Leu	Glu	Gly	Lys	Cys	Leu	Leu	Glu	Leu	Gly	Ala	Gly	Ile	Gly	Arg
		35					40					45			
Phe	Thr	Gly	Glu	Leu	Ala	Glu	Lys	Ala	Gly	Gln	Val	Ile	Ala	Leu	Asp
	50					55					60				
Phe	Ile	Glu	Ser	Ala	Ile	Lys	Lys	Asn	Glu	Val	Ile	Asn	Gly	His	Tyr
65					70					75					80
Lys	Asn	Val	Lys	Phe	Met	Cys	Ala	Asp	Val	Thr	Ser	Pro	Thr	Leu	Ser
				85					90					95	
Phe	Pro	Pro	His	Ser	Leu	Asp	Val	Ile	Phe	Ser	Asn	Trp	Leu	Leu	Met
			100					105					110		
Tyr	Leu	Ser	Asp	Glu	Glu	Val	Glu	Asn	Leu	Val	Glu	Arg	Met	Leu	Lys
	115						120					125			
Trp	Leu	Lys	Pro	Gly	Gly	Tyr	Ile	Phe	Phe	Arg	Glu	Ser	Cys	Phe	His
	130					135					140				
Gln	Ser	Gly	Asp	His	Lys	Arg	Lys	Ser	Asn	Pro	Thr	His	Tyr	Arg	Glu
145					150					155					160
Pro	Arg	Phe	Tyr	Thr	Lys	Ala	Phe	Lys	Glu	Cys	His	Leu	Gln	Asp	Gly
				165					170					175	
Ser	Gly	Asn	Ser	Tyr	Glu	Leu	Ser	Leu	Leu	Ser	Cys	Lys	Cys	Ile	Gly
			180					185					190		
Ala	Tyr	Val	Arg	Asn	Lys	Lys	Asn	Gln	Asn	Gln	Ile	Ser	Trp	Leu	Trp
	195						200					205			
Gln	Lys	Val	Asp	Ser	Lys	Asp	Asp	Lys	Gly	Phe	Gln	Arg	Phe	Leu	Asp
	210					215					220				
Thr	Ser	Gln	Tyr	Lys	Cys	Asn	Ser	Ile	Leu	Arg	Tyr	Glu	Arg	Val	Phe
225					230					235					240
Gly	Pro	Gly	Tyr	Val	Ser	Thr	Gly	Gly	Tyr	Glu	Thr	Thr	Lys	Glu	Phe
				245					250					255	
Val	Ser	Met	Leu	Asp	Leu	Lys	Pro	Gly	Gln	Lys	Val	Leu	Asp	Val	Gly
			260					265					270		

Cys Gly Ile Gly Gly Gly Asp Phe Tyr Met Ala Glu Thr Phe Asp Val
 275 280 285
 Glu Val Val Gly Phe Asp Leu Ser Val Asn Met Ile Ser Phe Ala Leu
 290 295 300
 Glu Arg Ser Ile Gly Leu Lys Cys Ala Val Glu Phe Glu Val Ala Asp
 305 310 315 320
 Cys Thr Lys Ile Asn Tyr Pro Asp Asn Ser Phe Asp Val Ile Tyr Ser
 325 330 335
 Arg Asp Thr Ile Leu His Ile Gln Asp Lys Pro Ala Leu Phe Arg Ser
 340 345 350
 Phe Tyr Lys Trp Leu Lys Pro Gly Gly Lys Val Leu Ile Ser Asp Tyr
 355 360 365
 Cys Lys Lys Ala Gly Pro Pro Ser Pro Glu Phe Ala Ala Tyr Ile Lys
 370 375 380
 Gln Arg Gly Tyr Asp Leu His Asp Val Lys Glu Tyr Gly Gln Met Leu
 385 390 395 400
 Lys Asp Ala Gly Phe Val Asp Val Leu Ala Glu Asp Arg Thr Glu Gln
 405 410 415
 Phe Ile Arg Val Leu Arg Lys Glu Leu Glu Thr Val Glu Lys Glu Lys
 420 425 430
 Asp Val Phe Ile Ser Asp Phe Ser Glu Glu Asp Tyr Asn Asp Ile Val
 435 440 445
 Gly Gly Trp Asn Asp Lys Leu Arg Arg Thr Ala Lys Gly Glu Gln Arg
 450 455 460
 Trp Gly Leu Phe Val Ala Lys Lys Lys
 465 470

<210> 41
 <211> 1251
 <212> DNA
 <213> Salsola komarovii

<220>

<221> CDS

<222> (1)..(933)

<400> 41

cag cca ttt ggc aca att aat gga tca ctt cgt gtt act gla caa ggt	48
Gln Pro Phe Gly Thr Ile Asn Gly Ser Leu Arg Val Thr Val Gln Gly	
1 5 10 15	
gag gtc att gaa caa tct ttt gga gag gag cac ttg tgt ttt aga aca	96
Glu Val Ile Glu Gln Ser Phe Gly Glu Glu His Leu Cys Phe Arg Thr	
20 25 30	
tta cag cgg tac aca gct gcc aca ctt gag cat gga atg cat cca cca	144
Leu Gln Arg Tyr Thr Ala Ala Thr Leu Glu His Gly Met His Pro Pro	
35 40 45	
atc tct cct aaa cca gaa tgg cgt gca ctt ttg gac gag atg gct gtt	192
Ile Ser Pro Lys Pro Glu Trp Arg Ala Leu Leu Asp Glu Met Ala Val	
50 55 60	
gtt gcc acc aag gaa tac cgc tct gtt gtt ttt cat gag cct cgc ttt	240
Val Ala Thr Lys Glu Tyr Arg Ser Val Val Phe His Glu Pro Arg Phe	
65 70 75 80	
gtc gag tac ttc cgc agt gct aca cca gag aca gag tat ggg cgt atg	288
Val Glu Tyr Phe Arg Ser Ala Thr Pro Glu Thr Glu Tyr Gly Arg Met	
85 90 95	
aat att gga agc cgt cct gca aag aga aag cca gga gga gga att gaa	336
Asn Ile Gly Ser Arg Pro Ala Lys Arg Lys Pro Gly Gly Gly Ile Glu	
100 105 110	
act ctg cgt gca att cct tgg ata ttt tcg tgg aca caa acc agg ttt	384
Thr Leu Arg Ala Ile Pro Trp Ile Phe Ser Trp Thr Gln Thr Arg Phe	
115 120 125	
cat tta cct gtg tgg ctt ggg gtt gga gca gct ttt aag cat gcc ctt	432
His Leu Pro Val Trp Leu Gly Val Gly Ala Ala Phe Lys His Ala Leu	
130 135 140	
gac aag gac att aag aat ctt tcg ata ctg aag gcc atg tat aat gag	480
Asp Lys Asp Ile Lys Asn Leu Ser Ile Leu Lys Ala Met Tyr Asn Glu	
145 150 155 160	
tgg ccg ttc ttc aga gtg act att gat ctg tta gaa atg gtt ttc act	528

Trp Pro Phe Phe Arg Val Thr Ile Asp Leu Leu Glu Met Val Phe Thr
 165 170 175
 aaa gga gac cct gga att gct gct tta tat gac aag ctt ctg gtg gca 576
 Lys Gly Asp Pro Gly Ile Ala Ala Leu Tyr Asp Lys Leu Leu Val Ala
 180 185 190
 gag gat ttg aag ccc ttt ggg gaa aag ttg agg aaa agt ttc gaa gat 624
 Glu Asp Leu Lys Pro Phe Gly Glu Lys Leu Arg Lys Ser Phe Glu Asp
 195 200 205
 acc aaa ctg ctt ctg ctt aag gtt gct ggg cac aag gag tta ctg gaa 672
 Thr Lys Leu Leu Leu Leu Lys Val Ala Gly His Lys Glu Leu Leu Glu
 210 215 220
 gga gat cct tac ttg aaa cag aga ctg cga ctt cgt gat cct tac att 720
 Gly Asp Pro Tyr Leu Lys Gln Arg Leu Arg Leu Arg Asp Pro Tyr Ile
 225 230 235 240
 aca acc ctt aat gtt ttc caa gca tat act ctg aag cgg atc cgt gat 768
 Thr Thr Leu Asn Val Phe Gln Ala Tyr Thr Leu Lys Arg Ile Arg Asp
 245 250 255
 ccc aat ttc cat gta gct gaa ggg cca cac tta tcc aag gaa gta ttg 816
 Pro Asn Phe His Val Ala Glu Gly Pro His Leu Ser Lys Glu Val Leu
 260 265 270
 gaa tca aac aat gct gag ctt gtg aag ctg aat cct act agt gag tat 864
 Glu Ser Asn Asn Ala Glu Leu Val Lys Leu Asn Pro Thr Ser Glu Tyr
 275 280 285
 cct cct ggc ctt gag gac acc ctt atc ttg acc atg aag ggt att gct 912
 Pro Pro Gly Leu Glu Asp Thr Leu Ile Leu Thr Met Lys Gly Ile Ala
 290 295 300
 gct ggc atg cag aac acc ggt taactgacac gtgtgtgcacg tctattgcaa 963
 Ala Gly Met Gln Asn Thr Gly
 305 310
 ctattcttca actccttctg gtttggggat ccgggtcgg agatagccat cgttggtagt 1023
 gtgtgtatg agcacctaat tgtattcaaa gtctgtatll caagtctatt gtatttgtat 1083
 ttgtgttctc tgtatgtttt tgtatttct acttaagggt gggttgtgtc acttgtgact 1143
 aataccggac tgtgtataaa atggttgttg tactgaagaa cagtltgttt tcttctacgt 1203

gagttatatt gatgatttta tcttttattt aaaaaaaaaa aaaaaaaaaa

1251

<210> 42

<211> 311

<212> PRT

<213> Salsola komarovii

<400> 42

Gln Pro Phe Gly Thr Ile Asn Gly Ser Leu Arg Val Thr Val Gln Gly
1 5 10 15

Glu Val Ile Glu Gln Ser Phe Gly Glu Glu His Leu Cys Phe Arg Thr
20 25 30

Leu Gln Arg Tyr Thr Ala Ala Thr Leu Glu His Gly Met His Pro Pro
35 40 45

Ile Ser Pro Lys Pro Glu Trp Arg Ala Leu Leu Asp Glu Met Ala Val
50 55 60

Val Ala Thr Lys Glu Tyr Arg Ser Val Val Phe His Glu Pro Arg Phe
65 70 75 80

Val Glu Tyr Phe Arg Ser Ala Thr Pro Glu Thr Glu Tyr Gly Arg Met
85 90 95

Asn Ile Gly Ser Arg Pro Ala Lys Arg Lys Pro Gly Gly Gly Ile Glu
100 105 110

Thr Leu Arg Ala Ile Pro Trp Ile Phe Ser Trp Thr Gln Thr Arg Phe
115 120 125

His Leu Pro Val Trp Leu Gly Val Gly Ala Ala Phe Lys His Ala Leu
130 135 140

Asp Lys Asp Ile Lys Asn Leu Ser Ile Leu Lys Ala Met Tyr Asn Glu
145 150 155 160

Trp Pro Phe Phe Arg Val Thr Ile Asp Leu Leu Glu Met Val Phe Thr
165 170 175

Lys Gly Asp Pro Gly Ile Ala Ala Leu Tyr Asp Lys Leu Leu Val Ala
180 185 190

Glu Asp Leu Lys Pro Phe Gly Glu Lys Leu Arg Lys Ser Phe Glu Asp
 195 200 205
 Thr Lys Leu Leu Leu Leu Lys Val Ala Gly His Lys Glu Leu Leu Glu
 210 215 220
 Gly Asp Pro Tyr Leu Lys Gln Arg Leu Arg Leu Arg Asp Pro Tyr Ile
 225 230 235 240
 Thr Thr Leu Asn Val Phe Gln Ala Tyr Thr Leu Lys Arg Ile Arg Asp
 245 250 255
 Pro Asn Phe His Val Ala Glu Gly Pro His Leu Ser Lys Glu Val Leu
 260 265 270
 Glu Ser Asn Asn Ala Glu Leu Val Lys Leu Asn Pro Thr Ser Glu Tyr
 275 280 285
 Pro Pro Gly Leu Glu Asp Thr Leu Ile Leu Thr Met Lys Gly Ile Ala
 290 295 300
 Ala Gly Met Gln Asn Thr Gly
 305 310

<210> 43
 <211> 637
 <212> DNA
 <213> Avicennia marina

<220>
 <221> CDS
 <222> (1).. (339)

<400> 43
 caa tac ttg gta aat gaa glg aag aaa act gtt cag ggg cgt gct caa 48
 Gln Tyr Leu Val Asn Glu Val Lys Lys Thr Val Gln Gly Arg Ala Gln
 1 5 10 15
 ctt ggt glg gaa gca ttt gct gat gcg ctt ctt glg gtt cca aag acg 96
 Leu Gly Val Glu Ala Phe Ala Asp Ala Leu Leu Val Val Pro Lys Thr
 20 25 30
 ctt gcc gag aac tct ggc ctt gat acc cag gat ttg att att gaa ctt 144
 Leu Ala Glu Asn Ser Gly Leu Asp Thr Gln Asp Leu Ile Ile Glu Leu

35	40	45	
acg gga gaa tat gaa aaa ggg aat gtg gla gga ctt aal cta cac aca	192		
Thr Gly Glu Tyr Glu Lys Gly Asn Val Val Gly Leu Asn Leu His Thr			
50 55 60			
gga gaa cct ata gal cct caa atg gag ggt atc ttt gac aat tat tcc	240		
Gly Glu Pro Ile Asp Pro Gln Met Glu Gly Ile Phe Asp Asn Tyr Ser			
65 70 75 80			
gtg aag cgt cag atc ata aac tca ggc ccc gtt att gca tct cag ctg	288		
Val Lys Arg Gln Ile Ile Asn Ser Gly Pro Val Ile Ala Ser Gln Leu			
85 90 95			
cta ctt gtc gac gag gtt att cgt gct ggt cgt aac atg cgt aaa ccg	336		
Leu Leu Val Asp Glu Val Ile Arg Ala Gly Arg Asn Met Arg Lys Pro			
100 105 110			
aat tagctttcac cctagttttt gtgatgttgg tgaagatggt aattttattt	389		
Asn			
aggtagggtc atggttccct ttgtttagcc taagcactat gtattcattg ccacttgaga	449		
tttgaatttt gatcattcagg cggttgaact ttctgccigt tacaatttgc accagaaatt	509		
attcgaccat gggtaigcat ctacttgtgt tgiaccigac ttggctaaagt tatttgaaga	569		
tacactcigt gctcagcaaa gaatttgaaa aaaaggaatt gatltcalca aaaaaaaaaa	629		
aaaaaaaa	637		

<210> 44

<211> 113

<212> PRT

<213> Avicennia marina

<400> 44

Gln Tyr Leu Val Asn Glu Val Lys Lys Thr Val Gln Gly Arg Ala Gln
1 5 10 15

Leu Gly Val Glu Ala Phe Ala Asp Ala Leu Leu Val Val Pro Lys Thr
20 25 30

Leu Ala Glu Asn Ser Gly Leu Asp Thr Gln Asp Leu Ile Ile Glu Leu
35 40 45

Thr Gly Glu Tyr Glu Lys Gly Asn Val Val Gly Leu Asn Leu His Thr
50 55 60

Gly Glu Pro Ile Asp Pro Gln Met Glu Gly Ile Phe Asp Asn Tyr Ser
65 70 75 80

Val Lys Arg Gln Ile Ile Asn Ser Gly Pro Val Ile Ala Ser Gln Leu
85 90 95

Leu Leu Val Asp Glu Val Ile Arg Ala Gly Arg Asn Met Arg Lys Pro
100 105 110

Asn

<210> 45

<211> 741

<212> DNA

<213> *Avicennia marina*

<220>

<221> CDS

<222> (3)..(293)

<400> 45

aa gag atc aat tgt ctt gaa tgg gag aac ttt gct ttc cat ccc agc 47
Glu Ile Asn Cys Leu Glu Trp Glu Asn Phe Ala Phe His Pro Ser
1 5 10 15

cca ctc att gtt ctt gtt ttt gaa aga tac aac agg gca agt gat aac 95
Pro Leu Ile Val Leu Val Phe Glu Arg Tyr Asn Arg Ala Ser Asp Asn
20 25 30

tgg aaa gct ttg aag gag ttg gaa aag gcg gca gaa gtt tac tgg aag 143
Trp Lys Ala Leu Lys Glu Leu Glu Lys Ala Ala Glu Val Tyr Trp Lys
35 40 45

gca aaa gat cga ctg cct cct cgg acg gtc aag ata gat ata aac atc 191
Ala Lys Asp Arg Leu Pro Pro Arg Thr Val Lys Ile Asp Ile Asn Ile
50 55 60

gaa agg gat tta gca tat gca ctc aag gtt aaa gaa tgc ccg cag ata 239
Glu Arg Asp Leu Ala Tyr Ala Leu Lys Val Lys Glu Cys Pro Gln Ile

65	70	75	
cig ttc tta cgc gga aac agg ala tta tac aga gag aaa ggt agc cca			287
Leu Phe Leu Arg Gly Asn Arg Ile Leu Tyr Arg Glu Lys Gly Ser Pro			
80	85	90	95
ttt ctc tga tat tgc a tgt acatc ag atctt tcaat ctc caccaga accaat tgc			343
Phe Leu			
ttt accat ca ttt ccagaaa tt agatc atc gga tga at tgc gtt caga tga tgc gcat ttt			403
ctattacaat gcaaaaaagc ct tgc tgc at cga tga tgc gct ttc tct t caccaca tca			463
ctgaagg tga ggt tgc aaaa tgg aatccag catc ag tca t agggaggac tga agct gta			523
cggagggaag tgg ttt aaaa tca gat tgg a tct t tga agt gggc ag tgg t gat tga aacg			583
ccaaaagt ttt ctg aggaata acct tgc tgg gat t tgc ag tga ac tgc tag taac ttc ttc			643
gcat gtaaaa ct agac ttc atcaat caac caccaacct ttt atgtata tgaaacctat			703
gaggt tga aa ttt ctat gta aaaaaaaaaa aaaaaaaaaa			741

<210> 46

<211> 97

<212> PRT

<213> Avicennia marina

<400> 46

Glu Ile Asn Cys Leu Glu Trp Glu Asn Phe Ala Phe His Pro Ser Pro
1 5 10 15

Leu Ile Val Leu Val Phe Glu Arg Tyr Asn Arg Ala Ser Asp Asn Trp
20 25 30

Lys Ala Leu Lys Glu Leu Glu Lys Ala Ala Glu Val Tyr Trp Lys Ala
35 40 45

Lys Asp Arg Leu Pro Pro Arg Thr Val Lys Ile Asp Ile Asn Ile Glu
50 55 60

Arg Asp Leu Ala Tyr Ala Leu Lys Val Lys Glu Cys Pro Gln Ile Leu
65 70 75 80

Phe Leu Arg Gly Asn Arg Ile Leu Tyr Arg Glu Lys Gly Ser Pro Phe

85

90

95

Leu

<210> 47

<211> 983

<212> DNA

<213> *Salsola komarovii*

<220>

<221> CDS

<222> (1)..(762)

<400> 47

atg	ttc	ctt	cat	cac	cac	ttt	tca	tct	tca	tct	tct	tct	ttt	ctt	ctt	48
Met	Phe	Leu	His	His	His	Phe	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Phe	Leu	Leu
1				5					10					15		

cgc	ttc	ttc	tct	cgc	cta	ata	ttc	ctt	tca	tct	gct	aat	ctt	tat	cat	96
Leu	Phe	Phe	Ser	Leu	Leu	Ile	Phe	Leu	Ser	Ser	Ala	Asn	Leu	Tyr	His	
			20					25					30			

cag	aat	caa	gga	tct	tgt	agc	gac	ttt	gaa	tca	gaa	cca	tca	atg	gct	144
Gln	Asn	Gln	Gly	Ser	Cys	Ser	Asp	Phe	Glu	Ser	Glu	Pro	Ser	Met	Ala	
		35					40					45				

act	ctt	ggt	gga	tig	cgc	gaa	tcc	cat	ggt	gct	tct	aat	gat	gct	gag	192
Thr	Leu	Gly	Gly	Leu	Arg	Glu	Ser	His	Gly	Ala	Ser	Asn	Asp	Ala	Glu	
	50					55					60					

att	gaa	acc	ctt	gct	cgc	ttt	gct	ggt	gat	gaa	cac	aac	aaa	aaa	gag	240
Ile	Glu	Thr	Leu	Ala	Arg	Phe	Ala	Val	Asp	Glu	His	Asn	Lys	Lys	Glu	
65					70				75						80	

aat	gca	tig	tig	gag	ttt	gca	agg	gtt	gta	aag	gca	aag	gaa	cag	gtg	288
Asn	Ala	Leu	Leu	Glu	Phe	Ala	Arg	Val	Val	Lys	Ala	Lys	Glu	Gln	Val	
				85					90					95		

ggt	gcg	ggt	aca	tig	cat	cac	ttc	act	atc	gaa	gca	att	gaa	gcg	ggc	336
Val	Ala	Gly	Thr	Leu	His	His	Phe	Thr	Ile	Glu	Ala	Ile	Glu	Ala	Gly	
			100					105					110			

aag	aag	aag	cgc	tac	gaa	gcg	aag	gtg	tgg	gtg	aag	cca	tgg	atg	aac	384
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Lys	Lys	Lys	Leu	Tyr	Glu	Ala	Lys	Val	Trp	Val	Lys	Pro	Trp	Met	Asn	
		115						120					125			
ttt	aag	gag	ctg	cag	gaa	ttt	aag	cat	gct	gat	gaa	icc	ccg	cca	atc	432
Phe	Lys	Glu	Leu	Gln	Glu	Phe	Lys	His	Ala	Asp	Glu	Ser	Pro	Ser	Ile	
		130						135					140			
act	ccg	icc	gac	ctc	ggc	gct	aat	aga	gaa	ggg	cat	ctc	gga	gga	tgg	480
Thr	Pro	Ser	Asp	Leu	Gly	Ala	Asn	Arg	Glu	Gly	His	Ser	Gly	Gly	Trp	
		145						150					155		160	
aaa	gat	gtg	ccg	gtc	cat	gac	ccg	gaa	gtg	caa	aat	gca	gca	aat	cat	528
Lys	Asp	Val	Pro	Val	His	Asp	Pro	Glu	Val	Gln	Asn	Ala	Ala	Asn	His	
					165						170				175	
gct	ctt	aag	acc	tgg	caa	caa	aga	icc	aac	icc	tta	ttt	ccg	tat	gaa	576
Ala	Leu	Lys	Thr	Leu	Gln	Gln	Arg	Ser	Asn	Ser	Leu	Phe	Pro	Tyr	Glu	
			180						185						190	
ctg	cag	gaa	gtt	gct	cat	gct	agg	gct	gag	gtt	ctg	gaa	gac	act	gcg	624
Leu	Gln	Glu	Val	Ala	His	Ala	Arg	Ala	Glu	Val	Leu	Glu	Asp	Thr	Ala	
			195						200						205	
aag	ttt	aac	ctg	cac	ctc	aag	gtg	aag	aga	gga	aac	aag	gat	gag	ttt	672
Lys	Phe	Asn	Leu	His	Leu	Lys	Val	Lys	Arg	Gly	Asn	Lys	Asp	Glu	Phe	
		210						215							220	
ttc	aat	gtg	gag	gtg	cac	aaa	aac	agc	gaa	gga	aac	tac	aac	ctt	aat	720
Phe	Asn	Val	Glu	Val	His	Lys	Asn	Ser	Glu	Gly	Asn	Tyr	Asn	Leu	Asn	
		225						230					235		240	
cag	atg	ggg	aac	gtt	gag	ccc	gag	gtt	gag	aaa	agt	agt	gtt			762
Gln	Met	Gly	Asn	Val	Glu	Pro	Glu	Val	Glu	Lys	Ser	Ser	Val			
				245						250						
tagactcggt	gaggggtgtg	taagtaactg	ttcgtaactt	ttcgtatggt	caggcaagta											822
tgtagtaagg	actagactac	tagtaactgt	aagtaactgt	gacttggttt	gagtaaaata											882
acctcgactt	tggttgcacc	atcatacttt	gtatgtttat	ggcttgttca	atgtatgtta											942
agtgaagatt	gtttgttga	tttaaaaaaa	aaaaaaaaaa	a												983

<210> 48

<211> 254

<212> PRT

<213> Salsola komarovii

<400> 48

Met	Phe	Leu	His	His	His	Phe	Ser	Ser	Ser	Ser	Ser	Ser	Phe	Leu	Leu
1				5					10					15	
Leu	Phe	Phe	Ser	Leu	Leu	Ile	Phe	Leu	Ser	Ser	Ala	Asn	Leu	Tyr	His
			20					25					30		
Gln	Asn	Gln	Gly	Ser	Cys	Ser	Asp	Phe	Glu	Ser	Glu	Pro	Ser	Met	Ala
		35					40					45			
Thr	Leu	Gly	Gly	Leu	Arg	Glu	Ser	His	Gly	Ala	Ser	Asn	Asp	Ala	Glu
	50					55					60				
Ile	Glu	Thr	Leu	Ala	Arg	Phe	Ala	Val	Asp	Glu	His	Asn	Lys	Lys	Glu
65					70				75						80
Asn	Ala	Leu	Leu	Glu	Phe	Ala	Arg	Val	Val	Lys	Ala	Lys	Glu	Gln	Val
				85					90					95	
Val	Ala	Gly	Thr	Leu	His	His	Phe	Thr	Ile	Glu	Ala	Ile	Glu	Ala	Gly
			100					105					110		
Lys	Lys	Lys	Leu	Tyr	Glu	Ala	Lys	Val	Trp	Val	Lys	Pro	Trp	Met	Asn
		115					120					125			
Phe	Lys	Glu	Leu	Gln	Glu	Phe	Lys	His	Ala	Asp	Glu	Ser	Pro	Ser	Ile
	130					135					140				
Thr	Pro	Ser	Asp	Leu	Gly	Ala	Asn	Arg	Glu	Gly	His	Ser	Gly	Gly	Trp
145					150					155					160
Lys	Asp	Val	Pro	Val	His	Asp	Pro	Glu	Val	Gln	Asn	Ala	Ala	Asn	His
				165					170					175	
Ala	Leu	Lys	Thr	Leu	Gln	Gln	Arg	Ser	Asn	Ser	Leu	Phe	Pro	Tyr	Glu
			180					185					190		
Leu	Gln	Glu	Val	Ala	His	Ala	Arg	Ala	Glu	Val	Leu	Glu	Asp	Thr	Ala
		195					200					205			
Lys	Phe	Asn	Leu	His	Leu	Lys	Val	Lys	Arg	Gly	Asn	Lys	Asp	Glu	Phe
	210					215					220				

Phe Asn Val Glu Val His Lys Asn Ser Glu Gly Asn Tyr Asn Leu Asn
 225 230 235 240

Gln Met Gly Asn Val Glu Pro Glu Val Glu Lys Ser Ser Val
 245 250

<210> 49
 <211> 543
 <212> DNA
 <213> Salsola komarovii

<220>
 <221> CDS
 <222> (3).. (389)

<400> 49
 aa aat aag gtt gac tta gct cga gat ttc acc ttc ata gac gac gtc 47
 Asn Lys Val Asp Leu Ala Arg Asp Phe Thr Phe Ile Asp Asp Val
 1 5 10 15
 gta aag ggg tgc tta ggt tca ctg gat tct tcc ggt aag agt acc ggt 95
 Val Lys Gly Cys Leu Gly Ser Leu Asp Ser Ser Gly Lys Ser Thr Gly
 20 25 30
 agc ggc ggt aaa aaa cgt ggg ccc gct ccg tac aga atc tac aac ttg 143
 Ser Gly Gly Lys Lys Arg Gly Pro Ala Pro Tyr Arg Ile Tyr Asn Leu
 35 40 45
 ggg aac act caa ccg gtc act gta ccg aca ctt gtc ggt atc cta gag 191
 Gly Asn Thr Gln Pro Val Thr Val Pro Thr Leu Val Gly Ile Leu Glu
 50 55 60
 aag cat ctc aaa gtt aag gcc aag aag aat gtg gtt gag atg ccc gga 239
 Lys His Leu Lys Val Lys Ala Lys Lys Asn Val Val Glu Met Pro Gly
 65 70 75
 aat ggt gac gtg ccc ttc aca cat gcg aat atc tct ttg gcc cga aaa 287
 Asn Gly Asp Val Pro Phe Thr His Ala Asn Ile Ser Leu Ala Arg Lys
 80 85 90 95
 gat ttc ggg tat aaa ccc act acc gat ttg caa acc ggg ttg aaa aag 335
 Asp Phe Gly Tyr Lys Pro Thr Thr Asp Leu Gln Thr Gly Leu Lys Lys
 100 105 110

111 gtt aga tgg tat ctc act tat tac ggc tac aac aac ggc aag cct 383
 Phe Val Arg Trp Tyr Leu Thr Tyr Tyr Gly Tyr Asn Asn Gly Lys Pro
 115 120 125

gla aat taatataaa atataagtaa tatTTTTTTT ctcTTTTTTT ataaattaca 439
 Val Asn

gaattatttt ttttgggtgg tttatgaatt ttgttggata atatggggat tctTTTTTTTc 499

taaaigggaa aaataagaat ccaaggaaaa aaaaaaaaaa aaaa 543

<210> 50

<211> 129

<212> PRT

<213> Salsola komarovii

<400> 50

Asn Lys Val Asp Leu Ala Arg Asp Phe Thr Phe Ile Asp Asp Val Val
 1 5 10 15

Lys Gly Cys Leu Gly Ser Leu Asp Ser Ser Gly Lys Ser Thr Gly Ser
 20 25 30

Gly Gly Lys Lys Arg Gly Pro Ala Pro Tyr Arg Ile Tyr Asn Leu Gly
 35 40 45

Asn Thr Gln Pro Val Thr Val Pro Thr Leu Val Gly Ile Leu Glu Lys
 50 55 60

His Leu Lys Val Lys Ala Lys Lys Asn Val Val Glu Met Pro Gly Asn
 65 70 75 80

Gly Asp Val Pro Phe Thr His Ala Asn Ile Ser Leu Ala Arg Lys Asp
 85 90 95

Phe Gly Tyr Lys Pro Thr Thr Asp Leu Gln Thr Gly Leu Lys Lys Phe
 100 105 110

Val Arg Trp Tyr Leu Thr Tyr Tyr Gly Tyr Asn Asn Gly Lys Pro Val
 115 120 125

Asn

<210> 51
 <211> 1219
 <212> DNA
 <213> *Saccharomyces japonica*

<220>
 <221> CDS
 <222> (2).. (871)

<400> 51
 c aca gga gca aac aaa gga ala gga ctt gaa cta tgc aaa caa cta gct 49
 Thr Gly Ala Asn Lys Gly Ile Gly Leu Glu Leu Cys Lys Gln Leu Ala
 1 5 10 15

 gct aaa gga gtt gta gta gtt ctc act tct aga gat gga aaa aga ggc 97
 Ala Lys Gly Val Val Val Val Leu Thr Ser Arg Asp Gly Lys Arg Gly
 20 25 30

 tta caa gct cat gaa aat ctc att aaa tct gga att aat cct gaa aat 145
 Leu Gln Ala His Glu Asn Leu Ile Lys Ser Gly Ile Asn Pro Glu Asn
 35 40 45

 ctt cac ttt cat cag ctc gat gtt act gac atc act agt att gct gct 193
 Leu His Phe His Gln Leu Asp Val Thr Asp Ile Thr Ser Ile Ala Ala
 50 55 60

 att gct ggt ttc atc aat tcc aaa ttc ggc aaa ctt gat atc ctg gtg 241
 Ile Ala Gly Phe Ile Asn Ser Lys Phe Gly Lys Leu Asp Ile Leu Val
 65 70 75 80

 aac aat gct gga att att gga gat atg gtt aac ttt gat gct tta ata 289
 Asn Asn Ala Gly Ile Ile Gly Asp Met Val Asn Phe Asp Ala Leu Ile
 85 90 95

 gca gca gga ttt ggc act cca aga gaa cag atc aat ctt gag gac agt 337
 Ala Ala Gly Phe Gly Thr Pro Arg Glu Gln Ile Asn Leu Glu Asp Ser
 100 105 110

 ccc ggg aca gta aca cag aca tat gag ctt acg aaa gaa tgc tta caa 385
 Pro Gly Thr Val Thr Gln Thr Tyr Glu Leu Thr Lys Glu Cys Leu Gln
 115 120 125

 aca aat tat tat gga gcg aaa aga acc gtt gaa gct ttg ctt ccg ctt 433
 Thr Asn Tyr Tyr Gly Ala Lys Arg Thr Val Glu Ala Leu Leu Pro Leu
 130 135 140

ctc aag tta tcc gat tct cca agg att gtc aat gtc tcc tct ttt cta 481
 Leu Lys Leu Ser Asp Ser Pro Arg Ile Val Asn Val Ser Ser Phe Leu
 145 150 155 160

gga agg ttg acg tat ata cca aat gag acg atc aga ggg gtc cta aga 529
 Gly Arg Leu Thr Tyr Ile Pro Asn Glu Thr Ile Arg Gly Val Leu Arg
 165 170 175

gat gcc gag agc ctt aca gaa gaa cga ata gat gag att ctg aat gac 577
 Asp Ala Glu Ser Leu Thr Glu Glu Arg Ile Asp Glu Ile Leu Asn Asp
 180 185 190

atg ctg agg gac ttc aaa gac tgt tca ttc aaa gag aag gga tgg cct 625
 Met Leu Arg Asp Phe Lys Asp Cys Ser Phe Lys Glu Lys Gly Trp Pro
 195 200 205

aaa aat ctg gca gcc tat ata gtt tca aag gcg gcc ttg agt gca tac 673
 Lys Asn Leu Ala Ala Tyr Ile Val Ser Lys Ala Ala Leu Ser Ala Tyr
 210 215 220

aca aga ata ctg gct aag aaa tac cca tca atc atg atc aac tgt att 721
 Thr Arg Ile Leu Ala Lys Lys Tyr Pro Ser Ile Met Ile Asn Cys Ile
 225 230 235 240

tgc cct ggc ttt gtc aaa act gac atc aat gga aac aca gga cac ttg 769
 Cys Pro Gly Phe Val Lys Thr Asp Ile Asn Gly Asn Thr Gly His Leu
 245 250 255

ccg gtt gaa gaa ggt gca gcg agt ctg gca agg tta gcg ttg atg ccc 817
 Pro Val Glu Glu Gly Ala Ala Ser Leu Ala Arg Leu Ala Leu Met Pro
 260 265 270

caa att tta cct tct gga cta ttc ttt cag aga act gaa gtt tct tgc 865
 Gln Ile Leu Pro Ser Gly Leu Phe Phe Gln Arg Thr Glu Val Ser Ser
 275 280 285

ttt gaa taaaacaatt tgcctatcca aaccaacacc acatattat gaagtttcca 921
 Phe Glu
 290

ttgttaggca tctttacgaa aaaaataaga calctgcaat actgttactg gaaaaigcaa 981

tgtacttttt tcatgtatgc atggcgcagt tatttatctt gactgcaaca ataagattct 1041

gtcttttcaa ggcactctaa ggaatgctga tglaccgttc tcaaacaagc agacaagtag 1101

acacglllga llglcalgic llcallecla caalcallll glllllglal gligagcatg ll6l

lllaactaal lacaagaglg laallaaagat caacilllal aaaaaaaaaa aaaaaaaaa 1219

<210> 52

<211> 290

<212> PRT

<213> Sueada japonica

<400> 52

Thr Gly Ala Asn Lys Gly Ile Gly Leu Glu Leu Cys Lys Gln Leu Ala
1 5 10 15

Ala Lys Gly Val Val Val Val Leu Thr Ser Arg Asp Gly Lys Arg Gly
20 25 30

Leu Gln Ala His Glu Asn Leu Ile Lys Ser Gly Ile Asn Pro Glu Asn
35 40 45

Leu His Phe His Gln Leu Asp Val Thr Asp Ile Thr Ser Ile Ala Ala
50 55 60

Ile Ala Gly Phe Ile Asn Ser Lys Phe Gly Lys Leu Asp Ile Leu Val
65 70 75 80

Asn Asn Ala Gly Ile Ile Gly Asp Met Val Asn Phe Asp Ala Leu Ile
85 90 95

Ala Ala Gly Phe Gly Thr Pro Arg Glu Gln Ile Asn Leu Glu Asp Ser
100 105 110

Pro Gly Thr Val Thr Gln Thr Tyr Glu Leu Thr Lys Glu Cys Leu Gln
115 120 125

Thr Asn Tyr Tyr Gly Ala Lys Arg Thr Val Glu Ala Leu Leu Pro Leu
130 135 140

Leu Lys Leu Ser Asp Ser Pro Arg Ile Val Asn Val Ser Ser Phe Leu
145 150 155 160

Gly Arg Leu Thr Tyr Ile Pro Asn Glu Thr Ile Arg Gly Val Leu Arg
165 170 175

Asp Ala Glu Ser Leu Thr Glu Glu Arg Ile Asp Glu Ile Leu Asn Asp

	180		185		190										
Met	Leu	Arg	Asp	Phe	Lys	Asp	Cys	Ser	Phe	Lys	Glu	Lys	Gly	Trp	Pro
	195		200		205										
Lys	Asn	Leu	Ala	Ala	Tyr	Ile	Val	Ser	Lys	Ala	Ala	Leu	Ser	Ala	Tyr
	210		215		220										
Thr	Arg	Ile	Leu	Ala	Lys	Lys	Tyr	Pro	Ser	Ile	Met	Ile	Asn	Cys	Ile
225			230		235									240	
Cys	Pro	Gly	Phe	Val	Lys	Thr	Asp	Ile	Asn	Gly	Asn	Thr	Gly	His	Leu
			245		250									255	
Pro	Val	Glu	Glu	Gly	Ala	Ala	Ser	Leu	Ala	Arg	Leu	Ala	Leu	Met	Pro
		260		265									270		
Gln	Ile	Leu	Pro	Ser	Gly	Leu	Phe	Phe	Gln	Arg	Thr	Glu	Val	Ser	Ser
	275		280		285										
Phe	Glu														
	290														

<210> 53
 <211> 1148
 <212> DNA
 <213> Sueada japonica

<220>
 <221> CDS
 <222> (3).. (848)

<400> 53
 ga agc agg ccg gat atc cat gtt gaa caa gct cat tca gat gat att 47
 Ser Arg Pro Asp Ile His Val Glu Gln Ala His Ser Asp Asp Ile
 1 5 10 15
 act ggg ttg aaa ttc tca tgt gat ggt cgt cat ctg ttg tct aga agt 95
 Thr Gly Leu Lys Phe Ser Cys Asp Gly Arg His Leu Leu Ser Arg Ser
 20 25 30
 ttt gat tgc aca ctt aag gtt tgg gac ttg cgc caa atg aag cgg tct 143
 Phe Asp Cys Thr Leu Lys Val Trp Asp Leu Arg Gln Met Lys Arg Ser
 35 40 45

cct aag glg ttt gat gaa tta cca aat cac tat gct caa acg aat gtc	191
Leu Lys Val Phe Asp Glu Leu Pro Asn His Tyr Ala Gln Thr Asn Val	
50 55 60	
lca ttt agt cca gat gag cag ctc atc ttg act ggt aca tct gla gaa	239
Ser Phe Ser Pro Asp Glu Gln Leu Ile Leu Thr Gly Thr Ser Val Glu	
65 70 75	
agg gat agc cca act gga gga ttg ttg tgc ttt tat gat cgg gaa aaa	287
Arg Asp Ser Pro Thr Gly Gly Leu Leu Cys Phe Tyr Asp Arg Glu Lys	
80 85 90 95	
cct gaa cta gla tca aaa gtt ggc att tct cct act tgc agt gtt gtg	335
Leu Glu Leu Val Ser Lys Val Gly Ile Ser Pro Thr Cys Ser Val Val	
100 105 110	
caa tgt gcc tgg cac cca agg ctg aat cag gtt ttt gcc act gct gga	383
Gln Cys Ala Trp His Pro Arg Leu Asn Gln Val Phe Ala Thr Ala Gly	
115 120 125	
aat aaa agc caa gga ggt aca cat gla ctc tat gat cca acc atg agt	431
Asn Lys Ser Gln Gly Gly Thr His Val Leu Tyr Asp Pro Thr Met Ser	
130 135 140	
gag aga ggt gct ctt glg tgt gtt gct cgt gca cca agg atg aaa tca	479
Glu Arg Gly Ala Leu Val Cys Val Ala Arg Ala Pro Arg Met Lys Ser	
145 150 155	
gtg gat gat ttt gag gtg cag ccg gtt ata cat aac cct cac gca ctt	527
Val Asp Asp Phe Glu Val Gln Pro Val Ile His Asn Pro His Ala Leu	
160 165 170 175	
ccc ttg ttc aga gat cag cca agc cgc aaa cgt caa aga gag aag att	575
Pro Leu Phe Arg Asp Gln Pro Ser Arg Lys Arg Gln Arg Glu Lys Ile	
180 185 190	
ctg aag gac cca ata aaa tcc cac aaa cca gag ctt cct atg tca gga	623
Leu Lys Asp Pro Ile Lys Ser His Lys Pro Glu Leu Pro Met Ser Gly	
195 200 205	
cct ggc cat ggt ggc aga act ggt aca tca tcg ggt agt ttg tta aca	671
Pro Gly His Gly Gly Arg Thr Gly Thr Ser Ser Gly Ser Leu Leu Thr	
210 215 220	
caa tat ctc ctc aag caa ggg ggc atg ttg aaa gag aca tgg atg gat	719

Gln Tyr Leu Leu Lys Gln Gly Gly Met Leu Lys Glu Thr Trp Met Asp
 225 230 235
 gaa gal ccc aga gaa gct att ctc aag tat gct gal gct gca gaa aag 767
 Glu Asp Pro Arg Glu Ala Ile Leu Lys Tyr Ala Asp Ala Ala Glu Lys
 240 245 250 255
 gat cca aag ttt att gcc ccg gct tat gct gag act cag ccc aag cca 815
 Asp Pro Lys Phe Ile Ala Pro Ala Tyr Ala Glu Thr Gln Pro Lys Pro
 260 265 270
 glc ttt gag gat tct gat aag gaa gat gaa gaa taattcaatc tttgcagttg 868
 Val Phe Glu Asp Ser Asp Lys Glu Asp Glu Glu
 275 280
 ttggattaat ttaatttgag aatattatc tgtgtatatt aatagccaat ttttcaggcg 928
 aatgataatgc ttctcacatt acatgctgag ttttatttgc tgctacagat tglagaigaa 988
 taggttaaig taaacacaag catagagatt agaatalaga aatgattctg tatccaaaac 1048
 acaattttat caccagaagg tatcaaaagc tgtattgact gttagagtaat gtcattaac 1108
 actttcactc cccaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1148

<210> 54
 <211> 282
 <212> PRT
 <213> Sueada japonica

<400> 54
 Ser Arg Pro Asp Ile His Val Glu Gln Ala His Ser Asp Asp Ile Thr
 1 5 10 15
 Gly Leu Lys Phe Ser Cys Asp Gly Arg His Leu Leu Ser Arg Ser Phe
 20 25 30
 Asp Cys Thr Leu Lys Val Trp Asp Leu Arg Gln Met Lys Arg Ser Leu
 35 40 45
 Lys Val Phe Asp Glu Leu Pro Asn His Tyr Ala Gln Thr Asn Val Ser
 50 55 60
 Phe Ser Pro Asp Glu Gln Leu Ile Leu Thr Gly Thr Ser Val Glu Arg
 65 70 75 80

Asp	Ser	Pro	Thr	Gly	Gly	Leu	Leu	Cys	Phe	Tyr	Asp	Arg	Glu	Lys	Leu
				85					90					95	
Glu	Leu	Val	Ser	Lys	Val	Gly	Ile	Ser	Pro	Thr	Cys	Ser	Val	Val	Gln
			100					105					110		
Cys	Ala	Trp	His	Pro	Arg	Leu	Asn	Gln	Val	Phe	Ala	Thr	Ala	Gly	Asn
			115				120					125			
Lys	Ser	Gln	Gly	Gly	Thr	His	Val	Leu	Tyr	Asp	Pro	Thr	Met	Ser	Glu
		130				135					140				
Arg	Gly	Ala	Leu	Val	Cys	Val	Ala	Arg	Ala	Pro	Arg	Met	Lys	Ser	Val
145					150					155					160
Asp	Asp	Phe	Glu	Val	Gln	Pro	Val	Ile	His	Asn	Pro	His	Ala	Leu	Pro
			165					170						175	
Leu	Phe	Arg	Asp	Gln	Pro	Ser	Arg	Lys	Arg	Gln	Arg	Glu	Lys	Ile	Leu
		180						185					190		
Lys	Asp	Pro	Ile	Lys	Ser	His	Lys	Pro	Glu	Leu	Pro	Met	Ser	Gly	Pro
		195					200					205			
Gly	His	Gly	Gly	Arg	Thr	Gly	Thr	Ser	Ser	Gly	Ser	Leu	Leu	Thr	Gln
	210					215					220				
Tyr	Leu	Leu	Lys	Gln	Gly	Gly	Met	Leu	Lys	Glu	Thr	Trp	Met	Asp	Glu
225					230					235					240
Asp	Pro	Arg	Glu	Ala	Ile	Leu	Lys	Tyr	Ala	Asp	Ala	Ala	Glu	Lys	Asp
			245						250					255	
Pro	Lys	Phe	Ile	Ala	Pro	Ala	Tyr	Ala	Glu	Thr	Gln	Pro	Lys	Pro	Val
		260						265					270		
Phe	Glu	Asp	Ser	Asp	Lys	Glu	Asp	Glu	Glu						
		275				280									

<210> 55
 <211> 1193
 <212> DNA
 <213> *Avicennia marina*

<220>

<221> CDS

<222> (3).. (815)

<400> 55

gi gca cct gag tta ctt ctt gga gca aag cat tat aca agt gct gtt	47
Ala Pro Glu Leu Leu Leu Gly Ala Lys His Tyr Thr Ser Ala Val	
1 5 10 15	
gac atg tgg gct gtg ggc tgc att ttt gct gag ctt ctg act cta aag	95
Asp Met Trp Ala Val Gly Cys Ile Phe Ala Glu Leu Leu Thr Leu Lys	
20 25 30	
cca cta ttt caa ggg caa gaa gta aaa ggg act tct aat cca ttt cag	143
Pro Leu Phe Gln Gly Gln Glu Val Lys Gly Thr Ser Asn Pro Phe Gln	
35 40 45	
ctt gat caa ctt gac aaa atc ttt aag gtc cta ggt cat ccc acg caa	191
Leu Asp Gln Leu Asp Lys Ile Phe Lys Val Leu Gly His Pro Thr Gln	
50 55 60	
gaa aag tgg ccc aca cta gcg aat ctt cca cat tgg cag tct gat gtg	239
Glu Lys Trp Pro Thr Leu Ala Asn Leu Pro His Trp Gln Ser Asp Val	
65 70 75	
caa cgt atc caa ggg ctc aaa tac gac aat act gga ctt tac aat gtt	287
Gln Arg Ile Gln Gly Leu Lys Tyr Asp Asn Thr Gly Leu Tyr Asn Val	
80 85 90 95	
gtt cat ctc tcc ccc aaa aat cca gca tat gac ctt ctc tca aag atg	335
Val His Leu Ser Pro Lys Asn Pro Ala Tyr Asp Leu Leu Ser Lys Met	
100 105 110	
ctt gag tat gat cct aga aaa aga ata aca gct aca caa gct ctt gag	383
Leu Glu Tyr Asp Pro Arg Lys Arg Ile Thr Ala Thr Gln Ala Leu Glu	
115 120 125	
cat gag tat ttt cgc atg gaa cct ttg ccg gga cgc aac gct ctg gta	431
His Glu Tyr Phe Arg Met Glu Pro Leu Pro Gly Arg Asn Ala Leu Val	
130 135 140	
cca cca cag cct ggg gag aaa att gtg aac tac cca aca cga cca gtg	479
Pro Pro Gln Pro Gly Glu Lys Ile Val Asn Tyr Pro Thr Arg Pro Val	
145 150 155	

gac aca aat act gat att gaa gga aca atc agc ctc cag ccc tct caa 527
 Asp Thr Asn Thr Asp Ile Glu Gly Thr Ile Ser Leu Gln Pro Ser Gln
 160 165 170 175

ccg gta tca tct ggg aat tct gtg tct ggg gcc cta gcc ggt cct cat 575
 Pro Val Ser Ser Gly Asn Ser Val Ser Gly Ala Leu Ala Gly Pro His
 180 185 190

gta atg caa aat aga tcc atg cct cgg cca atg ccc atg gtt ggc gtg 623
 Val Met Gln Asn Arg Ser Met Pro Arg Pro Met Pro Met Val Gly Val
 195 200 205

caa cgc atg caa cct cca ggg atc cca cac tat ggt ctt gct tct cag 671
 Gln Arg Met Gln Pro Pro Gly Ile Pro His Tyr Gly Leu Ala Ser Gln
 210 215 220

gca gga atg ggt gga gta aat cct ggt ggc atc cca att cag cgg gga 719
 Ala Gly Met Gly Gly Val Asn Pro Gly Gly Ile Pro Ile Gln Arg Gly
 225 230 235

gtt cct gct cag gct cat caa cag cag cag atg aga agg aaa gac cct 767
 Val Pro Ala Gln Ala His Gln Gln Gln Gln Met Arg Arg Lys Asp Pro
 240 245 250 255

gga atg ggg atg act gga tat cct cca caa cag aaa tca agg cgc ttt 815
 Gly Met Gly Met Thr Gly Tyr Pro Pro Gln Gln Lys Ser Arg Arg Phe
 260 265 270

tgagagtcg ggtggatttg gagcctaagt gggaggacaa atacacattc caatcaaat 875
 agaggaaacc ttaaatlaat ctccagtca gctgaaacga caccagtga accaaatgat 935
 ctgaccccat ttccaggatt gcatglatll attaggagga atacacgaat gaagattcga 995
 gtctagtgcc aaattatct aacatacctt catcatttgt tctactaca ttccgacgtt 1055
 atatgtttca actagtggaa gggtttctgc agtccacca tgtggcaca aatgattca 1115
 tagcatgcca agcaacacct tactgggtgt tactcaaggca atttctctat ttccaagcca 1175
 aaaaaaaaaa aaaaaaaaaa 1193

<210> 56
 <211> 271
 <212> PRT

<213> Avicennia marina

<400> 56

Ala Pro Glu Leu Leu Leu Gly Ala Lys His Tyr Thr Ser Ala Val Asp
1 5 10 15

Met Trp Ala Val Gly Cys Ile Phe Ala Glu Leu Leu Thr Leu Lys Pro
20 25 30

Leu Phe Gln Gly Gln Glu Val Lys Gly Thr Ser Asn Pro Phe Gln Leu
35 40 45

Asp Gln Leu Asp Lys Ile Phe Lys Val Leu Gly His Pro Thr Gln Glu
50 55 60

Lys Trp Pro Thr Leu Ala Asn Leu Pro His Trp Gln Ser Asp Val Gln
65 70 75 80

Arg Ile Gln Gly Leu Lys Tyr Asp Asn Thr Gly Leu Tyr Asn Val Val
85 90 95

His Leu Ser Pro Lys Asn Pro Ala Tyr Asp Leu Leu Ser Lys Met Leu
100 105 110

Glu Tyr Asp Pro Arg Lys Arg Ile Thr Ala Thr Gln Ala Leu Glu His
115 120 125

Glu Tyr Phe Arg Met Glu Pro Leu Pro Gly Arg Asn Ala Leu Val Pro
130 135 140

Pro Gln Pro Gly Glu Lys Ile Val Asn Tyr Pro Thr Arg Pro Val Asp
145 150 155 160

Thr Asn Thr Asp Ile Glu Gly Thr Ile Ser Leu Gln Pro Ser Gln Pro
165 170 175

Val Ser Ser Gly Asn Ser Val Ser Gly Ala Leu Ala Gly Pro His Val
180 185 190

Met Gln Asn Arg Ser Met Pro Arg Pro Met Pro Met Val Gly Val Gln
195 200 205

Arg Met Gln Pro Pro Gly Ile Pro His Tyr Gly Leu Ala Ser Gln Ala
210 215 220

Gly Met Gly Gly Val Asn Pro Gly Gly Ile Pro Ile Gln Arg Gly Val

225		230		235		240									
Pro	Ala	Gln	Ala	His	Gln	Gln	Gln	Gln	Met	Arg	Arg	Lys	Asp	Pro	Gly
				245					250					255	
Met	Gly	Met	Thr	Gly	Tyr	Pro	Pro	Gln	Gln	Lys	Ser	Arg	Arg	Phe	
			260					265						270	

<210> 57
 <211> 1195
 <212> DNA
 <213> Sueada japonica

<220>
 <221> CDS
 <222> (116).. (1195)

<400> 57
 gcaaaagtaa gagtgaaaga acacaaacca acttctatct ttcagctcaa atcaaatcca 60
 atagtggcaa aacaatagag ggcaaatctt catggcccaa ttcaaatctg glaaa atg 118
 Met
 1
 gct caa aag cat ttg aaa gaa ctt ctc aaa gaa gat caa gaa ccc ttt 166
 Ala Gln Lys His Leu Lys Glu Leu Leu Lys Glu Asp Gln Glu Pro Phe
 5 10 15
 cat tta aag gat tac att gca act aaa aaa tgt caa ctt ttg aag aag 214
 His Leu Lys Asp Tyr Ile Ala Thr Lys Lys Cys Gln Leu Leu Lys Lys
 20 25 30
 caa gaa tta gla gla ccc aaa tca aaa ctt caa ctc aaa aag cca aag 262
 Gln Glu Leu Val Val Pro Lys Ser Lys Leu Gln Leu Lys Lys Pro Lys
 35 40 45
 cca aaa cca att tca aaa agc act tca gtt ttg tgc aaa aat gct tgc 310
 Pro Lys Pro Ile Ser Lys Ser Thr Ser Val Leu Cys Lys Asn Ala Cys
 50 55 60 65
 ttt tta tct tta caa gaa tcc cct gac ctc aga aaa tcc ccc aaa cta 358
 Phe Leu Ser Leu Gln Glu Ser Pro Asp Leu Arg Lys Ser Pro Lys Leu
 70 75 80

ttt gat ttt cca cct tcc cct gtt tct aac aaa agc cca aac aga gla Phe Asp Phe Pro Pro Ser Pro Val Ser Asn Lys Ser Pro Asn Arg Val 85 90 95	406
ttc ctc aat gtt cct gct aaa act gct gct ctt ctt ctt gaa gct gct Phe Leu Asn Val Pro Ala Lys Thr Ala Ala Leu Leu Leu Glu Ala Ala 100 105 110	454
att cga att caa acc cac aaa tct aaa ccc aaa acc cag att aaa aat Ile Arg Ile Gln Thr His Lys Ser Lys Pro Lys Thr Gln Ile Lys Asn 115 120 125	502
tcg ggt ttt ggg cta ttc ggg tca atg tta aag cga tta aat ctt cga Ser Gly Phe Gly Leu Phe Gly Ser Met Leu Lys Arg Leu Asn Leu Arg 130 135 140 145	550
aat cgt acc caa aaa atc aag tca aaa aca gag gaa caa aac aga gga Asn Arg Thr Gln Lys Ile Lys Ser Lys Thr Glu Glu Gln Asn Arg Gly 150 155 160	598
tgc tct gtt ttg agg agt gtt gaa gaa gaa aaa act acc acc att tct Cys Ser Val Leu Arg Ser Val Glu Glu Glu Lys Thr Thr Thr Ile Ser 165 170 175	646
tct tct tca tct tca tct tct tca aca tca tgc tat tct tgc tgt tct Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Tyr Ser Ser Cys Ser 180 185 190	694
tgc aat gag agg tta agt agt ttg gat ttg gag agt tct agc agt gga Cys Asn Glu Arg Leu Ser Ser Leu Asp Leu Glu Ser Ser Ser Ser Gly 195 200 205	742
aga tca tta cat gat gaa gat gaa gat gaa gat gaa gat gat gaa ttt Arg Ser Leu His Asp Glu Asp Glu Asp Glu Asp Glu Asp Asp Glu Phe 210 215 220 225	790
gag ttt aca aat gtt tta aga gaa aat aat aat gat gat aaa aat gga Glu Phe Thr Asn Val Leu Arg Glu Asn Asn Asn Asp Asp Lys Asn Gly 230 235 240	838
ggt tat tat tca gga att tgc tta agt cct ttg agt cca ttt cgt ttt Gly Tyr Tyr Ser Gly Ile Cys Leu Ser Pro Leu Ser Pro Phe Arg Phe 245 250 255	886
gct ctt cat aaa aac tct tct cct gaa cgt tgc tct cct gct aaa tcc Ala Leu His Lys Asn Ser Ser Pro Glu Arg Cys Ser Pro Ala Lys Ser	934

260	265	270	
ccf gtl cgt tgc aaa tll gag ggt aal gct aaa tal gaa caa gaa agc			982
Pro Val Arg Cys Lys Phe Glu Gly Asn Ala Lys Tyr Glu Gln Glu Ser			
275	280	285	
lla ala aag tll gaa gac gaa gal gaa gaa gac aaa gag caa aat agc			1030
Leu Ile Lys Phe Glu Asp Glu Asp Glu Glu Asp Lys Glu Gln Asn Ser			
290	295	300	305
ccf gtl tcc gtg ctc gat cct cca ttc gag gat gat tac gat ggg cat			1078
Pro Val Ser Val Leu Asp Pro Pro Phe Glu Asp Asp Tyr Asp Gly His			
310	315	320	
gag gag gat agc tac gag gac aic gaa tgc agc tal gct tll gla caa			1126
Glu Glu Asp Ser Tyr Glu Asp Ile Glu Cys Ser Tyr Ala Phe Val Gln			
325	330	335	
aga gca caa caa gag tta ttg cac aga ctt cac cgg ttc cag aag cta			1174
Arg Ala Gln Gln Glu Leu Leu His Arg Leu His Arg Phe Gln Lys Leu			
340	345	350	
gcg gag ttg gac cca att gaa			1195
Ala Glu Leu Asp Pro Ile Glu			
355	360		
<210> 58			
<211> 360			
<212> PRT			
<213> Sueada japonica			
<400> 58			
Met Ala Gln Lys His Leu Lys Glu Leu Leu Lys Glu Asp Gln Glu Pro			
1	5	10	15
Phe His Leu Lys Asp Tyr Ile Ala Thr Lys Lys Cys Gln Leu Leu Lys			
20	25	30	
Lys Gln Glu Leu Val Val Pro Lys Ser Lys Leu Gln Leu Lys Lys Pro			
35	40	45	
Lys Pro Lys Pro Ile Ser Lys Ser Thr Ser Val Leu Cys Lys Asn Ala			
50	55	60	
Cys Phe Leu Ser Leu Gln Glu Ser Pro Asp Leu Arg Lys Ser Pro Lys			

65					70					75					80
Leu	Phe	Asp	Phe	Pro	Pro	Ser	Pro	Val	Ser	Asn	Lys	Ser	Pro	Asn	Arg
				85					90					95	
Val	Phe	Leu	Asn	Val	Pro	Ala	Lys	Thr	Ala	Ala	Leu	Leu	Leu	Glu	Ala
			100					105						110	
Ala	Ile	Arg	Ile	Gln	Thr	His	Lys	Ser	Lys	Pro	Lys	Thr	Gln	Ile	Lys
		115					120					125			
Asn	Ser	Gly	Phe	Gly	Leu	Phe	Gly	Ser	Met	Leu	Lys	Arg	Leu	Asn	Leu
		130					135					140			
Arg	Asn	Arg	Thr	Gln	Lys	Ile	Lys	Ser	Lys	Thr	Glu	Glu	Gln	Asn	Arg
145					150					155					160
Gly	Cys	Ser	Val	Leu	Arg	Ser	Val	Glu	Glu	Glu	Lys	Thr	Thr	Thr	Ile
				165					170					175	
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Thr	Ser	Ser	Tyr	Ser	Ser	Cys
			180					185					190		
Ser	Cys	Asn	Glu	Arg	Leu	Ser	Ser	Leu	Asp	Leu	Glu	Ser	Ser	Ser	Ser
		195					200					205			
Gly	Arg	Ser	Leu	His	Asp	Glu	Asp	Glu	Asp	Glu	Asp	Glu	Asp	Asp	Glu
	210					215					220				
Phe	Glu	Phe	Thr	Asn	Val	Leu	Arg	Glu	Asn	Asn	Asn	Asp	Asp	Lys	Asn
225					230					235					240
Gly	Gly	Tyr	Tyr	Ser	Gly	Ile	Cys	Leu	Ser	Pro	Leu	Ser	Pro	Phe	Arg
				245					250					255	
Phe	Ala	Leu	His	Lys	Asn	Ser	Ser	Pro	Glu	Arg	Cys	Ser	Pro	Ala	Lys
			260					265					270		
Ser	Pro	Val	Arg	Cys	Lys	Phe	Glu	Gly	Asn	Ala	Lys	Tyr	Glu	Gln	Glu
		275					280					285			
Ser	Leu	Ile	Lys	Phe	Glu	Asp	Glu	Asp	Glu	Glu	Asp	Lys	Glu	Gln	Asn
	290					295					300				
Ser	Pro	Val	Ser	Val	Leu	Asp	Pro	Pro	Phe	Glu	Asp	Asp	Tyr	Asp	Gly
305					310					315					320

His Glu Glu Asp Ser Tyr Glu Asp Ile Glu Cys Ser Tyr Ala Phe Val
325 330 335

Gln Arg Ala Gln Gln Glu Leu Leu His Arg Leu His Arg Phe Gln Lys
340 345 350

Leu Ala Glu Leu Asp Pro Ile Glu
355 360

<210> 59

<211> 1301

<212> DNA

<213> Salsola komarovii

<220>

<221> CDS

<222> (3).. (815)

<400> 59

gt gag gtt gac gat agc gtt aat agt cta cag gca gat gtt gac aac 47
Glu Val Asp Asp Ser Val Asn Ser Leu Gln Ala Asp Val Asp Asn
1 5 10 15

ctt tca att gag gaa cgc aga ttg gat gaa cag ata agg gaa atg caa 95
Leu Ser Ile Glu Glu Arg Arg Leu Asp Glu Gln Ile Arg Glu Met Gln
20 25 30

gaa aga ttg agg gaa atg agt gaa gat gat atc aat cag aag tgg ctt 143
Glu Arg Leu Arg Glu Met Ser Glu Asp Asp Ile Asn Gln Lys Trp Leu
35 40 45

ttt gta act gaa gaa gac ata aag ggt tta cct tgt ttt cag aat gaa 191
Phe Val Thr Glu Glu Asp Ile Lys Gly Leu Pro Cys Phe Gln Asn Glu
50 55 60

acc tta att gca att aaa gct cca cat gga aca act ttg gag gtt cca 239
Thr Leu Ile Ala Ile Lys Ala Pro His Gly Thr Thr Leu Glu Val Pro
65 70 75

gat cca gat gag gct gtc gat tat cct caa aga aga tac aag ata gtt 287
Asp Pro Asp Glu Ala Val Asp Tyr Pro Gln Arg Arg Tyr Lys Ile Val
80 85 90 95

ctt agg agc aca atg ggt cct att gat gla tat tta gtc agt caa ttt 335
 Leu Arg Ser Thr Met Gly Pro Ile Asp Val Tyr Leu Val Ser Gln Phe
 100 105 110

gaa gag aag ttt gag gag atc agt ggt gct gac ggt cca cta agt ata 383
 Glu Glu Lys Phe Glu Glu Ile Ser Gly Ala Asp Gly Pro Leu Ser Ile
 115 120 125

cca agt acc tca ggt gat gac aaa cac aca act gtt gca gct aag gaa 431
 Pro Ser Thr Ser Gly Asp Asp Lys His Thr Thr Val Ala Ala Lys Glu
 130 135 140

gaa agc aat ggc aat gag att gaa ata gaa gga caa ggg acc cat aga 479
 Glu Ser Asn Gly Asn Glu Ile Glu Ile Glu Gly Gln Gly Thr His Arg
 145 150 155

atc tgc tca gat tcc aac gct cag caa gac ttt gtg agt gga att atg 527
 Ile Cys Ser Asp Ser Asn Ala Gln Gln Asp Phe Val Ser Gly Ile Met
 160 165 170 175

aag ata gtg cct gaa gtt gat agt gat gca gat tac tgg ttg cta tct 575
 Lys Ile Val Pro Glu Val Asp Ser Asp Ala Asp Tyr Trp Leu Leu Ser
 180 185 190

gat gct gat gtt agc att act gac atg tgg gga act gat tct gga gtt 623
 Asp Ala Asp Val Ser Ile Thr Asp Met Trp Gly Thr Asp Ser Gly Val
 195 200 205

gaa tgg aat gaa tta ggg act ata cat gaa gac tat gcc gtg gct aat 671
 Glu Trp Asn Glu Leu Gly Thr Ile His Glu Asp Tyr Ala Val Ala Asn
 210 215 220

gtt ggc act tca cag cca caa agt cca cca aca agt gca aca gaa gtg 719
 Val Gly Thr Ser Gln Pro Gln Ser Pro Pro Thr Ser Ala Thr Glu Val
 225 230 235

ctt cca gct aac atg aca agc agg aga ttg aca tgg agt ttt gag aga 767
 Leu Pro Ala Asn Met Thr Ser Arg Arg Leu Thr Trp Ser Phe Glu Arg
 240 245 250 255

att gcc aar att cat tca aat ggt cac tat tgc ttg gaa gtg agg ctc 815
 Ile Ala Lys Ile His Ser Asn Gly His Tyr Cys Leu Glu Val Arg Leu
 260 265 270

taactttcta ttatcatcc tgggatttgg gtacgaaagt ctgccctigaa gatgcigtaa 875

caiglllgll allacaacig lglgaalcia glaagllggll agggllgagal lglliccigal 935
 cliallgcac agccggllgg gagagallga lcgclcaaca acigacaaaa llggggcailg 995
 llaacggala glalgcagll glaalillgl acalcacall lglgallll aglcaglaca 1055
 lcalaactag clcllccial acilcllcaa llglcaacig gaalagalll llagalllaal 1115
 lgaiclcic lllglalga aatglllcag gglaacaagc cagaaallaa aalggllllla 1175
 lglglaaaaa latalactia aallglllgl aggaaglllc lgalgggllg llggaillgc 1235
 lllaacaac acalcglala aggaaallcg lalcacaaal lcacaalgaa aaaaaaaaaa 1295
 aaaaaa 1301

<210> 60
 <211> 271
 <212> PRT
 <213> Salsola komarovii

<400> 60
 Glu Val Asp Asp Ser Val Asn Ser Leu Gln Ala Asp Val Asp Asn Leu
 1 5 10 15
 Ser Ile Glu Glu Arg Arg Leu Asp Glu Gln Ile Arg Glu Met Gln Glu
 20 25 30
 Arg Leu Arg Glu Met Ser Glu Asp Asp Ile Asn Gln Lys Trp Leu Phe
 35 40 45
 Val Thr Glu Glu Asp Ile Lys Gly Leu Pro Cys Phe Gln Asn Glu Thr
 50 55 60
 Leu Ile Ala Ile Lys Ala Pro His Gly Thr Thr Leu Glu Val Pro Asp
 65 70 75 80
 Pro Asp Glu Ala Val Asp Tyr Pro Gln Arg Arg Tyr Lys Ile Val Leu
 85 90 95
 Arg Ser Thr Met Gly Pro Ile Asp Val Tyr Leu Val Ser Gln Phe Glu
 100 105 110
 Glu Lys Phe Glu Glu Ile Ser Gly Ala Asp Gly Pro Leu Ser Ile Pro
 115 120 125

Ser Thr Ser Gly Asp Asp Lys His Thr Thr Val Ala Ala Lys Glu Glu
 130 135 140
 Ser Asn Gly Asn Glu Ile Glu Ile Glu Gly Gln Gly Thr His Arg Ile
 145 150 155 160
 Cys Ser Asp Ser Asn Ala Gln Gln Asp Phe Val Ser Gly Ile Met Lys
 165 170 175
 Ile Val Pro Glu Val Asp Ser Asp Ala Asp Tyr Trp Leu Leu Ser Asp
 180 185 190
 Ala Asp Val Ser Ile Thr Asp Met Trp Gly Thr Asp Ser Gly Val Glu
 195 200 205
 Trp Asn Glu Leu Gly Thr Ile His Glu Asp Tyr Ala Val Ala Asn Val
 210 215 220
 Gly Thr Ser Gln Pro Gln Ser Pro Pro Thr Ser Ala Thr Glu Val Leu
 225 230 235 240
 Pro Ala Asn Met Thr Ser Arg Arg Leu Thr Trp Ser Phe Glu Arg Ile
 245 250 255
 Ala Lys Ile His Ser Asn Gly His Tyr Cys Leu Glu Val Arg Leu
 260 265 270

<210> 61
 <211> 1032
 <212> DNA
 <213> Salsola komarovii

<220>
 <221> CDS
 <222> (1)..(732)

<400> 61
 cca caa cga aga ccc gac ccg gtc ccg aac ctt cac ggt cag ctt ttt 48
 Pro Gln Arg Arg Pro Asp Pro Val Pro Asn Leu His Gly Gln Leu Phe
 1 5 10 15
 caa cac cga aat cca cac cac cgt gac ctc cac ccc tgc cgt agc ccg 96
 Gln His Arg Asn Pro His His Arg Asp Leu His Pro Cys Arg Ser Pro

20	25	30	
gca alg ggt cca ctc cct ccg cag act cat ctg cgc tgg tat tcc ctc			144
Ala Met Gly Pro Leu Pro Pro Gln Thr His Leu Arg Trp Tyr Ser Leu			
35	40	45	
tcg cgc tac tcc ccc gtg atc ggc ctc ggc glc caa tgg aag ccc tcc			192
Ser Arg Tyr Ser Pro Val Ile Gly Leu Gly Val Gln Trp Lys Pro Ser			
50	55	60	
tcc acc tca gct gcc act ctt caa ctc agc atc gac aaa aag tgc ctc			240
Ser Thr Ser Ala Ala Thr Leu Gln Leu Ser Ile Asp Lys Lys Cys Leu			
65	70	75	80
atc ttc caa ctc tcc cac tcc ccc gcc atc ccc gcc acc ctc cgc gac			288
Ile Phe Gln Leu Ser His Ser Pro Ala Ile Pro Ala Thr Leu Arg Asp			
85	90	95	
ctc ctc ctc gac gat cgc glc acc ttc ttt ggt glc cac aac ggc cgt			336
Leu Leu Leu Asp Asp Arg Val Thr Phe Phe Gly Val His Asn Gly Arg			
100	105	110	
gcc cgc gac ctc ctc caa ggg tcc cac cat gag ctc gac glc aac aat			384
Ala Arg Asp Leu Leu Gln Gly Ser His His Glu Leu Asp Val Asn Asn			
115	120	125	
ctg gtt gat ctt gcc gag gag gaa aat ggt cat tac ttg aag tgg tcc			432
Leu Val Asp Leu Ala Glu Glu Glu Asn Gly His Tyr Leu Lys Trp Ser			
130	135	140	
atg gaa gac atg gct gaa gat gtg ttg ggc ttt tgt ggg gla cac aaa			480
Met Glu Asp Met Ala Glu Asp Val Leu Gly Phe Cys Gly Val His Lys			
145	150	155	160
ccc agg aag gtt atg tta agt ggt tgg gat cag tat tgc ttg tct aat			528
Pro Arg Lys Val Met Leu Ser Gly Trp Asp Gln Tyr Cys Leu Ser Asn			
165	170	175	
gac cag gtt cag tat gct tgt gtt gat gct tac gtt tct ctt cgt ctt			576
Asp Gln Val Gln Tyr Ala Cys Val Asp Ala Tyr Val Ser Leu Arg Leu			
180	185	190	
gct cga gct tat ggg tac cac cgt ctc gat cac gat gat gat tat gat			624
Ala Arg Ala Tyr Gly Tyr His Arg Leu Asp His Asp Asp Asp Tyr Asp			
195	200	205	

gac cai gac gac gal gal aac gac cac acc gal gal gal iac gal gac 672
 Asp His Asp Asp Asp Asp Asn Asp His Thr Asp Asp Asp Tyr Asp Asp
 210 215 220
 gtt tac gac cgc aat aia ggc tct gal gal gal ggt tat gal gcc gal 720
 Val Tyr Asp Arg Asn Ile Gly Ser Asp Asp Asp Gly Tyr Asp Ala Asp
 225 230 235 240
 gal gal cga cga tgalcaattt ggactagact tctttattgg aagggtccga 772
 Asp Asp Arg Arg
 tcatcatgcc agtctaatla caaagagaca agaaataaaa atgatgatca aaaaaagaag 832
 tcaatccata tacgtaatit tcatlgcaat alcaattitg aggtgtttla ttattggcct 892
 glaataatag ttttatltiaa taatagcact atagatctca tctaacctt tactttattgg 952
 gctttatgcgc tgtatgtcca ataaccaagt ttaattttat tcatgatctg atgattactg 1012
 caaaaaaaaa aaaaaaaaaa 1032

<210> 62
 <211> 244
 <212> PRT
 <213> Salsola komarovii

<400> 62
 Pro Gln Arg Arg Pro Asp Pro Val Pro Asn Leu His Gly Gln Leu Phe
 1 5 10 15
 Gln His Arg Asn Pro His His Arg Asp Leu His Pro Cys Arg Ser Pro
 20 25 30
 Ala Met Gly Pro Leu Pro Pro Gln Thr His Leu Arg Trp Tyr Ser Leu
 35 40 45
 Ser Arg Tyr Ser Pro Val Ile Gly Leu Gly Val Gln Trp Lys Pro Ser
 50 55 60
 Ser Thr Ser Ala Ala Thr Leu Gln Leu Ser Ile Asp Lys Lys Cys Leu
 65 70 75 80
 Ile Phe Gln Leu Ser His Ser Pro Ala Ile Pro Ala Thr Leu Arg Asp
 85 90 95

Leu Leu Leu Asp Asp Arg Val Thr Phe Phe Gly Val His Asn Gly Arg
 100 105 110
 Ala Arg Asp Leu Leu Gln Gly Ser His His Glu Leu Asp Val Asn Asn
 115 120 125
 Leu Val Asp Leu Ala Glu Glu Glu Asn Gly His Tyr Leu Lys Trp Ser
 130 135 140
 Met Glu Asp Met Ala Glu Asp Val Leu Gly Phe Cys Gly Val His Lys
 145 150 155 160
 Pro Arg Lys Val Met Leu Ser Gly Trp Asp Gln Tyr Cys Leu Ser Asn
 165 170 175
 Asp Gln Val Gln Tyr Ala Cys Val Asp Ala Tyr Val Ser Leu Arg Leu
 180 185 190
 Ala Arg Ala Tyr Gly Tyr His Arg Leu Asp His Asp Asp Asp Tyr Asp
 195 200 205
 Asp His Asp Asp Asp Asp Asn Asp His Thr Asp Asp Asp Tyr Asp Asp
 210 215 220
 Val Tyr Asp Arg Asn Ile Gly Ser Asp Asp Asp Gly Tyr Asp Ala Asp
 225 230 235 240
 Asp Asp Arg Arg

<210> 63
 <211> 1029
 <212> DNA
 <213> Mesembryanthemum crystallinum

<220>
 <221> CDS
 <222> (3)..(824)

<400> 63
 ca caI atc agc cac atc cac tta all ccc cac agl ctt agl ctc tta 47
 His Ile Ser His Ile His Leu Ile Pro His Ser Leu Ser Leu Leu
 1 5 10 15

gac acc cat ctt agt ctt aag cct ctc atg gcc acc gcg gla ttc tca	95
Asp Thr His Leu Ser Leu Lys Pro Leu Met Ala Thr Ala Val Phe Ser	
20 25 30	
cct tct gcc ctt cta tcc acc tcc aca tcc acc tca aca acc cct ctt	143
Pro Ser Ala Leu Leu Ser Thr Ser Thr Ser Thr Ser Thr Thr Pro Leu	
35 40 45	
aaa gct ccc ccc ttg gcc tta acc aag acc cac gla acg atc cca tca	191
Lys Ala Pro Pro Leu Ala Leu Thr Lys Thr His Val Thr Ile Pro Ser	
50 55 60	
tca tca aag cca ccc cta acc aat tta act acc agt tta act gct glc	239
Ser Ser Lys Pro Pro Leu Thr Asn Leu Thr Thr Ser Leu Thr Ala Val	
65 70 75	
gcc aca gct gct gcc ata atc ctg tcc aca acc cct cca tcc ttt gct	287
Ala Thr Ala Ala Ala Ile Ile Leu Ser Thr Thr Pro Pro Ser Phe Ala	
80 85 90 95	
gat gat ttg cag aca aat gca tac aac att tac tac ggc act gct gca	335
Asp Asp Leu Gln Thr Asn Ala Tyr Asn Ile Tyr Tyr Gly Thr Ala Ala	
100 105 110	
agt gca gcc aat tat gga ggc tac ggt ggc aat tcc aac aag aaa gat	383
Ser Ala Ala Asn Tyr Gly Gly Tyr Gly Gly Asn Ser Asn Lys Lys Asp	
115 120 125	
tca gct gag tac ata tat gac glc cct gca ggt tgg aaa gag aga cta	431
Ser Ala Glu Tyr Ile Tyr Asp Val Pro Ala Gly Trp Lys Glu Arg Leu	
130 135 140	
gla tca aaa gtt gag aag ggt acc aat gga aca gat agt gag ttc ttc	479
Val Ser Lys Val Glu Lys Gly Thr Asn Gly Thr Asp Ser Glu Phe Phe	
145 150 155	
aac ccc aag aag aag aca gag cga gag tac ctt acc tac ctt gct ggt	527
Asn Pro Lys Lys Lys Thr Glu Arg Glu Tyr Leu Thr Tyr Leu Ala Gly	
160 165 170 175	
att agg caa cta ggt ccc aaa gaa gtg atc ctc aac aac tta gca ctc	575
Ile Arg Gln Leu Gly Pro Lys Glu Val Ile Leu Asn Asn Leu Ala Leu	
180 185 190	
tca gat gtg aac ctg caa gat caa att tcc agt gca gac tct gtg aca	623
Ser Asp Val Asn Leu Gln Asp Gln Ile Ser Ser Ala Asp Ser Val Thr	

195	200	205	
tca gaa gag agg aaa gal gac aag gga cag gtt tac tat gat tat gag			671
Ser Glu Glu Arg Lys Asp Asp Lys Gly Gln Val Tyr Tyr Asp Tyr Glu			
210	215	220	
att gct gga gct ggt tca cac agt ttg ata tcg gta aca tgt gcc agg			719
Ile Ala Gly Ala Gly Ser His Ser Leu Ile Ser Val Thr Cys Ala Arg			
225	230	235	
aac aag cta tat gcg cat ttt gtt agc gca cca aca ccc gaa tgg aat			767
Asn Lys Leu Tyr Ala His Phe Val Ser Ala Pro Thr Pro Glu Trp Asn			
240	245	250	255
cgg gat caa gat atg ctg agg cac atc cac aac tca ttt aca aca gtc			815
Arg Asp Gln Asp Met Leu Arg His Ile His Asn Ser Phe Thr Thr Val			
260	265	270	
ggg tca ttc tagaaagigt ataigataat cattataga gatgtcagag			864
Gly Ser Phe			
aggcatacat ttgaatgtac ttctgatgag ctggacttct tgaictatgt aacattgtaa			924
cgaaaaatct ttttgggtta tcagaaacct agtgagtgtc tgaaacttgc aatgagaaac			984
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<212> PRT

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His Ile Ser His Ile His Leu Ile Pro His Ser Leu Ser Leu Leu Asp

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5

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15

Thr His Leu Ser Leu Lys Pro Leu Met Ala Thr Ala Val Phe Ser Pro

20

25

30

Ser Ala Leu Leu Ser Thr Ser Thr Ser Thr Ser Thr Pro Leu Lys

35

40

45

Ala Pro Pro Leu Ala Leu Thr Lys Thr His Val Thr Ile Pro Ser Ser

50

55

60

Ser Lys Pro Pro Leu Thr Asn Leu Thr Thr Ser Leu Thr Ala Val Ala
 65 70 75 80
 Thr Ala Ala Ala Ile Ile Leu Ser Thr Thr Pro Pro Ser Phe Ala Asp
 85 90 95
 Asp Leu Gln Thr Asn Ala Tyr Asn Ile Tyr Tyr Gly Thr Ala Ala Ser
 100 105 110
 Ala Ala Asn Tyr Gly Gly Tyr Gly Gly Asn Ser Asn Lys Lys Asp Ser
 115 120 125
 Ala Glu Tyr Ile Tyr Asp Val Pro Ala Gly Trp Lys Glu Arg Leu Val
 130 135 140
 Ser Lys Val Glu Lys Gly Thr Asn Gly Thr Asp Ser Glu Phe Phe Asn
 145 150 155 160
 Pro Lys Lys Lys Thr Glu Arg Glu Tyr Leu Thr Tyr Leu Ala Gly Ile
 165 170 175
 Arg Gln Leu Gly Pro Lys Glu Val Ile Leu Asn Asn Leu Ala Leu Ser
 180 185 190
 Asp Val Asn Leu Gln Asp Gln Ile Ser Ser Ala Asp Ser Val Thr Ser
 195 200 205
 Glu Glu Arg Lys Asp Asp Lys Gly Gln Val Tyr Tyr Asp Tyr Glu Ile
 210 215 220
 Ala Gly Ala Gly Ser His Ser Leu Ile Ser Val Thr Cys Ala Arg Asn
 225 230 235 240
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 Ser Phe

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